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From: Jiang, Dong
Sent: Thursday, August 22, 2002 2:10 PM
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Priority: 8/14/99
Chen (Genetech)

Please search SEQ ID NO:3

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no art.

Please send results on paper to Dong Jiang in 10D-08 (mail stop CM1-10D19).
Thank you very much.

Dong Jiang (78243)
703-305-1345
U.S. Patent and Trademark Office
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dong.jiang@uspto.gov
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Searcher: Point of Contact
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Date Completed: 8/25/02
Searcher Prep/Review: _____
Clerical: _____
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TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 23, 2002, 16:00:49 ; Search time 29.85 Seconds
(without alignments)
733.050 Million cell updates/sec

Title: US-09-854-208-3
Perfect score: 1073
Sequence: 1 MTLPLGLFLTLWHTCLAHH.....FHTFTHVPVGCTVLP RSV 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*
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2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
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20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	100.0	197	21	AA18911
2	1073	100.0	197	21	AA18911
3	1073	100.0	197	21	AA18911
4	1073	100.0	197	21	AA18911
5	1073	100.0	197	21	AA18911
6	1073	100.0	197	21	AA18911
7	1073	100.0	197	21	AA18911
8	1073	100.0	197	21	AA18911
9	1073	100.0	197	21	AA18911
10	1073	100.0	197	21	AA18911
11	1073	100.0	197	21	AA18911

12	1063	99.1	227	22	AAE08676	Human interleukin
13	1061	98.9	227	22	AAE08680	Human interleukin
14	1061	98.9	227	22	AAE08682	Human interleukin
15	1060	98.8	227	22	AAE08681	Human interleukin
16	1060	98.8	227	22	AAE08685	Human interleukin
17	1059	98.7	227	22	AAE08684	Human interleukin
18	1059	98.7	227	22	AAE08687	Human interleukin
19	1058	98.6	227	22	AAE08679	Human interleukin
20	1058	98.6	227	22	AAE08683	Human interleukin
21	1058	98.6	227	22	AAE08686	Human interleukin
22	1055	98.3	227	22	AAE08690	Human interleukin
23	1054	98.2	227	22	AAE08688	Human interleukin
24	1054	98.2	227	22	AAE08689	Human interleukin
25	1054	98.2	227	22	AAE08691	Human interleukin
26	1054	98.2	227	22	AAE08693	Human interleukin
27	1054	98.2	227	22	AAE08695	Human interleukin
28	1054	98.2	227	22	AAE08697	Human interleukin
29	1054	98.2	227	22	AAE08699	Human interleukin
30	1054	98.2	227	22	AAE08701	Human interleukin
31	1054	98.2	227	22	AAE08703	Human interleukin
32	1053	98.1	227	22	AAE08692	Human interleukin
33	1053	98.1	227	22	AAE08694	Human interleukin
34	1053	98.1	227	22	AAE08696	Human interleukin
35	1053	98.1	227	22	AAE08698	Human interleukin
36	1053	98.1	227	22	AAE08700	Human interleukin
37	1053	98.1	227	22	AAE08702	Human interleukin
38	1034	96.4	223	22	AAE08677	Human mature inter
39	459	42.8	87	21	AA53890	Partial amino acid
40	459	42.8	87	21	AA53890	Human interleukin
41	446	41.6	123	21	AA07601	A human interleukin
42	446	41.6	123	21	AA07683	A human interleukin
43	199	18.5	202	21	AA07595	A human interleukin
44	199	18.5	202	21	AA07689	A human interleukin
45	199	18.5	202	21	AA07653	Human transforming

ALIGNMENTS

RESULT 1	
AA18911	AA18911 standard; Protein; 197 AA.
ID	AA18911 standard; Protein; 197 AA.
XX	
AC	AA18911;
XX	
DT	08-FEB-2001 (first entry)
XX	
DE	A novel polypeptide designated PRO1122.
XX	
KW	Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;
KW	PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;
KW	PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5950; PRO6030;
KW	PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;
KW	insulinemia; kidney disorder; Bergers disease; nephropathy;
KW	Schonelein-Henoch purpura; celiac disease; dermatitis herpetiformis;
KW	Crohn's disease.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..18
FT	/note= "signal peptide"
FT	3..25
FT	/note= "leucine zipper pattern"
FT	32..38
FT	/note= "N-myristoylation site"
FT	55..61
FT	/note= "N-myristoylation site"
FT	112..121
FT	/note= "tyrosine kinase phosphorylation site"
FT	133..139
XX	
PN	WO200056889-A2.

XX 28-SEP-2000.
XX
XX
XX 01-MAR-2000; 2000WO-US05601.
XX
XX 23-MAR-1999; 99US-0125774.
XX 23-MAR-1999; 99US-0125778.
XX 24-MAR-1999; 99US-0125826.
XX 31-MAR-1999; 99US-0127035.
XX 05-APR-1999; 99US-0127706.
XX 21-APR-1999; 99US-0130359.
XX 27-APR-1999; 99US-0131270.
XX 27-APR-1999; 99US-0131272.
XX 27-APR-1999; 99US-0131291.
XX 04-MAY-1999; 99US-0132371.
XX 04-MAY-1999; 99US-0132379.
XX 04-MAY-1999; 99US-0132383.
XX 25-MAY-1999; 99US-0135750.
XX 08-JUN-1999; 99US-0138166.
XX 20-JUL-1999; 99US-0144791.
XX 03-AUG-1999; 99US-0146970.
XX 09-DEC-1999; 99US-0170262.

(GETH) GENENTECH INC.

Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
Stewart TA, Watanabe CK, Wood WI, Zhang Z;

WPI: 2000-628263/60.
N-PSDB; AAA96338.

Novel secreted and transmembrane polypeptides useful for diagnosing
tumour in a mammal, for identifying agonists and antagonists of the
polypeptide and for therapeutic use

Claim 12; Fig 6; 222pp; English.

The present sequence represents a secreted or transmembrane polypeptide.
The specification describes polypeptides designated PRO1484, PRO4334,
PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
PRO4356, PRO4352, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,
PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
useful for diagnosing tumour in a mammal. The polypeptides, their
agonists and antagonists are useful treating a condition associated with
expression or activity of the polypeptide. Conditions treated include
obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are
capable of inducing proliferation of mammalian kidney mesangial cells
and are therefore useful for treating kidney disorders associated with
decreased mesangial cell function such as Berger's disease or other
nephropathies associated with Schönlein-Henoch purpura, celiac disease,
dermatitis herpetiformis or Crohn's disease. The nucleic acids may be used
to generate transgenic animals for use in development and screening of
therapeutically useful reagents and also for chromosome identification
and tissue typing.

Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 21; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLETLWLHTCLAHHDPSLRGPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60
DB 1 mtlplglflftwlhtclahhdpslrghphshgtphcysaeelp1gqapphllargakwgq 60
QY 61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLADTHQRSISPRYRVDTDEDY 120
DB 61 alpvalvssleashaashrgrherpsattqcpvlrpeevleadthqrsispryrvdtdedry 120
QY 121 POKLAFAECLRCGCDIARTGRETAAALNSVRLQLSLVLRPPCRSDGSLPTPGAFAFHT 180
DB 121 pqlkafaeclrcgcidartgretaalnsrvllqslvlrrppcsrdgsglptpgafafht 180

QY 181 EFTIHPVGCTCVLPFRSV 197
DB 181 efihipvgctcvlprsv 197
RESULT 2
AAB07602
ID AAB07602 standard; Protein; 197 AA.
XX
XX AAB07602;
XX
XX 07-NOV-2000 (first entry)
XX
XX A human interleukin (IL) 171 polypeptide.
XX
XX Interleukin: IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;
KW IL-177; IL-171; cell proliferation; cancer.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Peptide 1..17
FT Protein /note= "signal peptide"
FT /note= "mature protein"
XX
XX WO200042188-A2.
XX
XX 20-JUL-2000.
XX
XX 10-JAN-2000; 2000WO-US00006.
XX
XX 11-JAN-1999; 99US-0228822.
XX
XX (SCHE) SCHERING CORP.
XX
XX Gorman DM, Bazan JF, Kastelein RA;
XX
XX WPI: 2000-466130/40.
XX
XX N-PSDB; AAA58991.
XX
XX New isolated polynucleotide encoding a mammalian Interleukin-17 like
PT protein used to identify genes for homologous proteins -
XX
XX Disclosure; Page 20-21; 111pp; English.

XX The present sequence represents an interleukin-171 (IL-171) polypeptide.
XX The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a
XX member of a new group of interleukins, IL-170 polypeptides. The members
XX comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170
XX protein can be used to treat abnormal proliferation e.g. cancer
XX or degenerative conditions. Antibodies can be used in diagnostic
XX methods to detect over production of IL-170 protein in cells or body
XX fluids.
XX
XX Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 21; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLETLWLHTCLAHHDPSLRGPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60
DB 1 mtlplglflftwlhtclahhdpslrghphshgtphcysaeelp1gqapphllargakwgq 60
QY 61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLADTHQRSISPRYRVDTDEDY 120
DB 61 alpvalvssleashaashrgrherpsattqcpvlrpeevleadthqrsispryrvdtdedry 120
QY 121 POKLAFAECLRCGCDIARTGRETAAALNSVRLQLSLVLRPPCRSDGSLPTPGAFAFHT 180

Db	121	pqlafaeclrgcidartgretaaalnsvllqslvlvrrrrpcsdrgslptpgafafht	180
QY	181	EFIHPVPGCTCVLPVPSV 197	
Db	181	efihvpvgctcvlprsv 197	
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AA07684			
ID	AA07684	standard; Protein; 197 AA.	
AC	AA07684;		
XX			
DT	07-NOV-2000	(first entry)	
XX			
DE	A human interleukin-171 polypeptide.		
XX			
KW	Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;		
KW	IL-174; IL-176; IL-177; cell proliferation; cancer.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..17	
FT		/note= "signal peptide"	
FT	Protein	18..197	
FT		/note= "mature protein"	
FT	Modified-site	55..57	
FT		/note= "putative glycosylation site"	
XX			
PN	WO200042187-A1.		
XX			
PD	20-JUL-2000.		
XX			
PF	10-JAN-2000; 2000WO-US000005.		
XX			
PR	11-JAN-1999; 99US-0229402.		
XX			
PA	(SCHE) SCHERING CORP.		
PI	Gorman DM, Bazan JF, Kastelein RA;		
XX			
DR	WPI; 2000-476060/41.		
DR	N-PSDB; AAA59149.		
XX			
PT	New DNA sequence encoding a mammalian homolog of CTLA-8, designated		
PT	interleukin-171 (IL-171), useful for recombinant production of IL-171		
PT	which can be used for treating conditions associated with abnormal		
PT	physiology or development -		
XX			
PS	Claim 11; Page 10-11; 11lpp; English.		
XX			
CC	The present sequence represents an interleukin (IL)-171 polypeptide.		
CC	It is a mammalian homologue of the cytokine designated CTLA-8 (also		
CC	referred to as IL-17). The specification also describes homologues		
CC	IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA		
CC	sequence encoding IL-171 is useful for identifying genes, mRNA and		
CC	cDNA molecules which code for related or homologous proteins. The		
CC	IL-171 protein, antibodies against IL-171, and compounds which have		
CC	binding affinity to IL-171 are useful in treatment of conditions		
CC	associated with abnormal physiology or development, including abnormal		
CC	proliferation, e.g. cancerous conditions, or degenerative conditions.		
CC	The IL-171 protein can be used in kits and assay methods for identifying		
CC	compounds that selectively bind to IL-171.		
XX			
SQ	Sequence 197 AA;		
Query Match	100.0%;	Score 1073;	DB 21; Length 197;
Best Local Similarity	100.0%;	Pred. No. 4.6e-109;	
Matches 197; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
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Db	1	mtllpglflftwlhtclahdpdslgrhpshtgtpchysaeelpgqapphllargakwq	60
QY	61	ALPVALVSSLEASHRHRPSATTQCPLRPEEVLADTHORSISPWRYRVDTDDEY	120
Db	61	alpvalvssleashrhrpsattqcplrpeevleadtorsispwryrvdtdey	120
QY	121	PKLAFAECLRCGICDARTGRETAAALNSVRLQLSLVLRRRPCSRDGLPTPGAFAFHT	180
Db	121	pqlafaeclrgcidartgretaaalnsvllqslvlvrrrrpcsdrgslptpgafafht	180
QY	181	EFIHPVPGCTCVLPVPSV 197	
Db	181	efihvpvgctcvlprsv 197	
RESULT	4		
AA092238			
ID	AA092238	standard; Protein; 197 AA.	
XX			
AC	AA092238;		
XX			
DT	10-AUG-2000	(first entry)	
XX			
DE	Human interleukin-17 (IL-17) homologue.		
XX			
KW	Interleukin 17; IL-17; haematopoiesis; chemotherapy; cytostatic;		
KW	antianemic; cardiant; hemostatic; anti-inflammatory; anti-HIV.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..18	
FT		/label= signal_peptide	
FT	Protein	19..197	
FT		/label= mature_protein	
XX			
PN	WO200020593-A1.		
XX			
PD	13-APR-2000.		
XX			
PF	30-SEP-1999; 99WO-US22678.		
XX			
PR	02-OCT-1998; 98US-0102883.		
PR	01-DEC-1998; 98US-0110405.		
PR	11-JUN-1999; 99US-0138910.		
XX			
PA	(ELIL) LILLY & CO ELI.		
XX			
PI	Glasebrook AL, Su EW, Wei J, Liu L;		
XX			
DR	WPI; 2000-303778/26.		
DR	N-PSDB; AAA09153.		
XX			
PT	Nucleic acid encoding an interleukin-17 (IL-17) homolog polypeptide		
PT	which enhances hematopoiesis, useful for treating e.g. anemia,		
PT	thrombocytopenia, viral and bacterial infections		
XX			
PS	Claim 16; Page 92-93; 11lpp; English.		
XX			
CC	Interleukin 17 (IL-17) stimulates hematopoiesis and production of		
CC	neutrophils, granulocytes, or platelets, this may be useful during		
CC	chemotherapy. IL-17 homologues have at least one activity selected		
CC	from induction of cytotoxic T cells, induction of lymphokine-activated		
CC	killer cell proliferation or a B or T cell stimulation. The IL-17		
CC	homologue may also be used to treat viral or bacterial infections,		
CC	immune related diseases, anemia, leukemia, thrombocytopenia, uremia,		
CC	Von Willebrand disease, postoperative cardiovascular dysfunction,		
CC	treatment of AIDS (acquired immune deficiency syndrome)-related bone		
CC	marrow failure, and inflammatory diseases of the gastrointestinal		
CC	system, joints, and lungs.		
XX			
SQ	Sequence 197 AA;		

Query Match 100.0%; Score 1073; DB 21; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLFTLWLTCLAHDPSSLRHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60
Db 1 mtlplgllflitwhltclahdpslrghpshgtphcysaeelpigqapphllargakwgq 60
QY 61 ALPVALVSSLEAASHRGHERPSATTQCPVLRPEEVLEADTHORSISPWRYRVDTDDEY 120
Db 61 alpvalvssleashaashrgherpsattqcpvlrpeevleadthgrsispwryrvdtddedry 120
QY 121 PQLAFACELCRGICDARTGRETAAALNSVRLQLSLVLRPPCSRDCGSLPTPCAFAFHT 180
Db 121 pqlafaeclrcgcidartgretaalnsrvllqslvlrrrpscdgsglptpgafafht 180
QY 181 EFTHVPVGCCTCVLPRSV 197
Db 181 efthvpvgctcvlprsv 197

RESULT 5
AA44460
ID AA44460 standard; Protein; 197 AA.
XX
AC AA44460;
XX
DT 27-MAR-2000 (first entry)
XX
DE Human Interleukin 17C, PRO1122 polypeptide.
XX
KW Interleukin; IL-17C; PRO1122 polypeptide; clone DNA62377-1381-1; UN0561;
KW cytokine IL-17; cytotoxic T-lymphocyte-associated antigen 8; CTLA-8;
KW hybridisation probe; antagonist; degenerative cartilaginous disorder;
KW agonist; diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT Protein 19..197
FT /label= Signal_peptide
FT /label= Mature_IL-17C_polypeptide
FT /note= "Used to treat degenerative cartilaginous
FT disorder"
FT Misc-difference 109 /note= "Conserved Trp residue"
FT Misc-difference 129 /note= "Conserved Cys residue"
FT Misc-difference 134 /note= "Conserved Cys residue"
FT Misc-difference 163 /note= "Conserved Cys residue"
FT Misc-difference 189 /note= "Conserved Cys residue"
FT Misc-difference 191 /note= "Conserved Cys residue"
XX
PN W09960127-A2.
XX
PD 25-NOV-1999.
XX
PF 14-MAY-1999; 99WO-US10733.
XX
PR 15-MAY-1998; 98US-0085579.
PR 23-DEC-1998; 98US-0113621.
XX
PA (GETH) GENENTECH INC.
XX
PI Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WI;
XX

DR WPI; 2000-116314/10.
XX N-PSDB; AA229728.
XX New polypeptides designated PRO1031 and PRO1122 used to treat a
PT degenerative cartilaginous disorder -
XX Claim 23; Fig 3; 14lpp; English.
PS
XX The present sequence is the human PRO1122 polypeptide, also referred to
CC as UN0561, and as interleukin-17C (IL-17C), encoded by
CC clone DNA62377-1381-1. This sequence has identity with the
CC cytokine IL-17 and cytotoxic T-lymphocyte-associated antigen 8 (CTLA-8)
CC and has leucine zipper pattern. PRO1122 is expressed in pancreas, small
CC intestine, stomach and testis also. It shares about 26-28% amino acid
CC identity with IL-17 and IL-17B. The entire coding region of IL-17C can
CC be used as hybridisation probe. The PRO1122 polypeptide, agonist or
CC antagonist, is used to diagnose and treat a degenerative cartilaginous
CC disorder.
XX
SQ Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 21; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLFTLWLTCLAHDPSSLRHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60
Db 1 mtlplgllflitwhltclahdpslrghpshgtphcysaeelpigqapphllargakwgq 60
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Db 61 alpvalvssleashaashrgherpsattqcpvlrpeevleadthgrsispwryrvdtddedry 120
QY 121 PQLAFACELCRGICDARTGRETAAALNSVRLQLSLVLRPPCSRDCGSLPTPCAFAFHT 180
Db 121 pqlafaeclrcgcidartgretaalnsrvllqslvlrrrpscdgsglptpgafafht 180
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Db 181 efthvpvgctcvlprsv 197

RESULT 6
AA53892
ID AA53892 standard; Protein; 197 AA.
XX
AC AA53892;
XX
DT 13-MAR-2000 (first entry)
XX
DE Amino acid sequence of human interleukin-21.
XX
KW Human; interleukin-22; IL-22; IL-21; immune system disorder;
KW Immune cell chemotaxis; haematopoietic cell disorder;
KW haemostatic activity; thrombolytic activity; autoimmune disorder; asthma;
KW respiratory problem; organ rejection; graft-versus-host disease; GVHD;
KW inflammation; hyperproliferative disorder; tissue regeneration;
KW embryonic stem cell differentiation; embryonic stem cell proliferation;
KW haematopoietic lineage; allergic asthma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT /note= "signal peptide"
FT Domain 34..40
FT /note= "conserved domain V"
FT Domain 63..68
FT /note= "conserved domain VI"
FT Domain 104..109
FT /note= "conserved domain VII"
FT Domain 113..121

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FT      /note= "conserved domain II"
FT      156..162
FT      /note= "conserved domain III"
FT      185..192
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XX      WO9961617-A1.
PN      02-DEC-1999.
XX      27-MAY-1999; 99WO-US11644..
XX      29-MAY-1998; 98US-0087340.
PR      10-SEP-1998; 98US-0099805.
PR      30-APR-1999; 99US-0131965.
XX      (HUMA-) HUMAN GENOME SCI INC.
PA      Ruben SM, Ebner R;
XX      WPI; 2000-072622/06.
XX      N-PSDB; AAZ36836.
DR      Novel polynucleotides used to develop products for treating e.g. immune
XX      disorders, blood disorders, autoimmune disorders, allergies,
XX      inflammation, hyperproliferative disorders or infections
XX      Claim 26; Fig 6A-B; 170pp; English.
XX      The present sequence represents a human interleukin-21 (IL-21)
XX      protein. The specification also describes IL-22 polynucleotides and
XX      polypeptides. The IL-21 polynucleotide was isolated from a cDNA library
XX      of apoptotic T-cells. IL-21 and IL-22 may be useful in treating
XX      deficiencies or disorders of the immune system, by activating or
XX      inhibiting the proliferation, differentiation, or mobilization
XX      (chemotaxis) of immune cells, treating or detecting deficiencies or
XX      disorders of haematopoietic cells, to modulate haemostatic or
XX      thrombolytic activity, in treating or detecting autoimmune disorders,
XX      treating asthma (particularly allergic asthma) or other respiratory
XX      problems, to treat and/or prevent organ rejection or graft-versus-host
XX      disease (GVHD), to modulate inflammation, to treat or detect
XX      hyperproliferative disorders, to treat or detect infectious agents, to
XX      differentiate, proliferate and attract cells, leading to the
XX      regeneration of tissues, IL-21 and IL-22 may also increase or decrease
XX      the differentiation or proliferation of embryonic stem cells and
XX      haematopoietic lineage, may be used to modulate mammalian
XX      characteristics.
XX      Sequence 197 AA;

Query Match      100.08; Score 1073; DB 21; Length 197;
Best Local Similarity 100.08; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTLPLGLFLTLWHLTCLAHHDPSLRGHPSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ 60
Db      1 mtlpgllfltlwhtclahhdpslrghpshtphcysaeelpgqapphllargakwgq 60

QY      61 ALPVALVSSLEASHRGHERPSATTQCPLRPEEVLEADTHQRSTSPWRYRVDTDEDRY 120
Db      61 alpvalvssleashrgherpsattqcplrpeevleadthqrsispwryrvdtdedry 120

QY      121 POKLFAECLRCGCDARTGRTAALNSVRLLOSLVLVLRRCSDRGSLPFGAFHT 180
Db      121 pklfaeclrcgdcartgretaalnsvrlqlslvlvrrpcsdrgslptpgafafht 180

QY      181 EFHVPVGCVCVLPVRSV 197
Db      181 efhvpvgctcvlprsv 197

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RESULT      7
AAG66121
ID      AAG66121 standard; Protein; 197 AA.
XX      AC      AAG66121;
XX      DT      13-MAR-2002 (first entry)
XX      DE      Human Interleukin (IL)-21 amino acid sequence.
XX      KW      Interleukin; IL-21; IL-22; immunosuppressive; cytostatic; thrombolytic;
XX      KW      antiinflammatory; antibacterial; gene therapy; human.
XX      OS      Homo sapiens.
XX      FH      Key
XX      FT      Peptide
XX      FT      1..18
XX      FT      /note= "signal peptide"
XX      FT      Protein
XX      FT      19..197
XX      FT      /note= "mature protein"
XX      FT      Domain
XX      FT      34..40
XX      FT      /note= "conserved domain V"
XX      FT      Domain
XX      FT      63..68
XX      FT      /note= "conserved domain VI"
XX      FT      Domain
XX      FT      104..109
XX      FT      /note= "conserved domain VII"
XX      FT      Domain
XX      FT      113..121
XX      FT      /note= "conserved domain I"
XX      FT      Domain
XX      FT      129..134
XX      FT      /note= "conserved domain II"
XX      FT      Domain
XX      FT      156..162
XX      FT      /note= "conserved domain III"
XX      FT      Domain
XX      FT      185..192
XX      FT      /note= "conserved domain IV"
XX      US2001023070-A1.
XX      20-SEP-2001.
XX      08-DEC-2000; 2000US-0731816.
XX      29-MAY-1998; 98US-087340P.
XX      30-APR-1999; 99US-131965P.
XX      09-DEC-1999; 99US-169837P.
XX      27-MAY-1999; 99US-0320713.
XX      27-MAY-1999; 99WO-US11644.
XX      (EBNE/) EBNER R.
XX      (RUBE/) RUBEN S M.
XX      Ebner R, Ruben SM;
XX      WPI; 2001-638470/73.
XX      N-PSDB; AAI67878.
XX      New interleukin-21 and interleukin-22 polynucleotides and polypeptides,
XX      useful for treating, preventing or diagnosing e.g. disorders of
XX      hematopoietic cells, autoimmune disorders, or hyperproliferative
XX      diseases
XX      Claim 26; Fig 6A-B; 87pp; English.
XX      The invention relates to novel human proteins designated interleukin
XX      (IL)-21 and IL-22. The IL-21 and IL-22 polynucleotides can be used in
XX      linkage analysis as a marker for those specific chromosome, in chromosome
XX      mapping, to control gene expression through triple helix formation or
XX      antisense DNA or RNA, in gene therapy, in identifying individuals from
XX      minute biological samples, as an alternative to restriction fragment
XX      length polymorphism (RFLP) analysis, as polymorphic markers for forensic
XX      purposes, as molecular weight markers, or as diagnostic probes. IL-21 and
XX      IL-22 polypeptides can be used to treat, prevent or diagnose diseases of
XX      the immune system by activating or inhibiting the proliferation,

```

CC differentiation or mobilization of immune cells, disorders of
CC hematopoietic cells (e.g. ataxia, human immunodeficiency virus (HIV)
CC infection, anemia, thrombocytopenia), autoimmune disorders (e.g. Grave's
CC disease, systemic lupus erythematosus, ophthalmia), graft versus host
CC disease, inflammation, hyperproliferative disorders, or infectious
CC diseases. The polypeptides are useful for generating antibodies, which
CC can be used to treat, inhibit or prevent diseases or conditions
CC associated with aberrant expression and/or activity of IL-21 or IL-22.
CC The present sequence represents the amino acid sequence of human IL-21.
XX
SQ Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 22; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLFTLWLTCLAHHDPSLRGPHSHGTPHCYSABEELPLGQAPPHLLARGAKWGQ 60
Db 1 mtlplgllfltlwltclahhdpslrghphshgtphcysaeelpgqapphllargakwgq 60
QY 61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLADTHORSISPWRYRYVDTDEDY 120
Db 61 alpvalvssleaaashrgrherpsattqcpvlrpeevleadthgrspswryryvdtddedry 120
QY 121 POKLAFACELRCGICDARTGRETAALNSVRLQLSLVLRPPCRSDGSLPTPCAFAPHT 180
Db 121 pqklafaeclrcgcidartgreetaalnsvrlqlslvlrrppcsrdgslptpgafafht 180
QY 181 EFTHVPVGCVCVLPVRSV 197
Db 181 eftlvpgvgtcvlprsv 197

RESULT 8
AAU29247
ID AAU29247 standard; Protein; 197 AA.
XX
AC AAU29247;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #224.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06520.

XX
PR 01-MAR-2000; 2000WO-US03601.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 30-MAR-2000; 2000US-193053P.
PR 29-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.

PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-064848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX
(GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WL, Zhang Z;
XX
DR WPI; 2001-602746/68.
DR N-PSDB; AAS46148.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -
XX
PS Claim 11; Fig 448; 774pp; English.
XX
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.
XX
SQ Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 22; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLFTLWLTCLAHHDPSLRGPHSHGTPHCYSABEELPLGQAPPHLLARGAKWGQ 60
Db 1 mtlplgllfltlwltclahhdpslrghphshgtphcysaeelpgqapphllargakwgq 60
QY 61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLADTHORSISPWRYRYVDTDEDY 120
Db 61 alpvalvssleaaashrgrherpsattqcpvlrpeevleadthgrspswryryvdtddedry 120
QY 121 POKLAFACELRCGICDARTGRETAALNSVRLQLSLVLRPPCRSDGSLPTPCAFAPHT 180
Db 121 pqklafaeclrcgcidartgreetaalnsvrlqlslvlrrppcsrdgslptpgafafht 180

QY 181 EFIHVPVGTCTVLPKRSV 197
 PT |||||||||||||||
 Db 181 efihvpvgctcvlprsv 197

RESULT 9
 AAU04951
 ID AAU04951 standard; Protein; 197 AA.
 XX
 AC AAU04951;
 DT 24-OCT-2001 (first entry)
 XX
 DE Human Interleukin 17C ligand, IL-17C.
 KW Human; Interleukin-17C ligand; IL-17C; agonist; antagonist;
 KW PRO1122; DNA 62377-1381-1; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;
 KW allergic disease; asthma; demyelinating disease;
 KW degenerative cartilaginous disorder; transplantation associated disease.
 XX
 OS Homo sapiens.

Key	Location/Qualifiers
Key	1..18
Peptide	/label= Signal_peptide
Region	3..25
Region	/note= "Leucine zipper pattern"
Protein	19..197
Region	/label= Mature_IL_17C
Region	32..38
Region	/note= "N-myristoylation site"
Region	55..61
Region	/note= "N-myristoylation site"
Region	99..125
Region	/note= "Region homologous to IL-17"
Region	112..121
Region	/note= "Tyrosine kinase phosphorylation site"
Region	133..139
Region	/note= "N-myristoylation site"

WO200146420-A2.

28-JUN-2001.

20-DEC-2000; 2000WO-US34956.

23-DEC-1999; 99US-0172096.
 30-DEC-1999; 99WO-US31274.
 11-JAN-2000; 2000US-0175481.
 18-FEB-2000; 2000WO-US04341.
 02-MAR-2000; 2000WO-US05841.
 21-MAR-2000; 2000US-0191007.
 21-MAR-2000; 2000WO-US07532.
 02-JUN-2000; 2000WO-US15264.
 22-JUN-2000; 2000US-0213087.
 24-AUG-2000; 2000US-0644848.
 24-AUG-2000; 2000WO-US23328.
 24-OCT-2000; 2000US-0242837.
 10-NOV-2000; 2000WO-US30873.
 28-NOV-2000; 2000US-0253646.
 01-DEC-2000; 2000WO-US32678.

(GETH) GENENTECH INC.

XX Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;
 PI Gurney AL, Li H, Hillan KJ, Tamas D, Van Lookeren M, Vandlen RL;
 PI Watanabe CK, Williams PM, Wood WI, Yansura DG;
 DR WPI; 2001-451708/48.
 DR N-PSDB; AAS09510.
 XX

PT Novel PRO polypeptides homologous to interleukin-17, useful for the
 PT diagnosis and treatment of immune related disease e.g. rheumatoid
 XX arthritis and diabetes -
 PS Claim 10; Fig 4; 188pp; English.
 XX
 CC The sequence is PRO1122 which is the human Interleukin 17C ligand,
 CC IL-17C, encoded by DNA 62377-1381-1. A composition
 CC containing ant/agonists to the PRO polypeptides or individual components
 CC are useful for treating a mammal with an immune related disease, e.g.
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthritis, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease, an autoimmune or immune-mediated skin
 CC disease, contact dermatitis, an allergic disease e.g. food
 CC hypersensitivity, asthma, a transplantation associated disease, or a
 CC chronic inflammatory demyelinating polyneuropathy. Treating a
 CC degenerative cartilaginous disorder comprises administering a PRO1031 or
 CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous
 CC examples of the diseases and disorders are given in the specification.
 XX
 XX Sequence 197 AA;

Query Match	100.0%	Score 1073;	DB 22;	Length 197;
Best Local Similarity	100.0%	Pred. No. 4.6e-109;		
Matches 197;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	MTLLPGLLFTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQ	60		
Db 1	mtllpgllftwlhtclahhdpslrghphshgtpchysaeelpgqapphllargakwgq	60		
QY 61	ALPVALVSSLEAASHRGHRERPSATTCQCVLPREEVLEADTHQRSISPRYRVDTDEDRY	120		
Db 61	alpvavssleashrgrherpsattqcpvlrpeevleadthqrsispryrvdtdedry	120		
QY 121	PKLFAECLRCGCDARTGRTAALNSVRLQLSLVLRRCRDSGLPTPGAFAFHT	180		
Db 121	pkklfaeclrcgcidartgretaalnsvrlqlslvlrrpcsdrgslptpgafafht	180		
QY 181	EFIHVPVGTCTVLPKRSV 197			
Db 181	efihvpvgctcvlprsv 197			

RESULT 10

AAU44485
 ID AAY44485 standard; Protein; 206 AA.
 XX
 AC AAY44485;
 XX
 DT 27-MAR-2000 (first entry)
 XX
 DE Human Interleukin 17C with C-terminal Gly(His)8 tag, IL-17C.his.
 XX
 KW Interleukin; IL-17C.his; PRO1122 polypeptide; clone DNA62377-1381-1;
 KW immunoprecipitation; IL-17 receptor extracellular domain; IL-17R ECD;
 KW cytokine IL-17; hybridisation probe; antagonist; Gly(His)8 tag; agonist;
 KW degenerative cartilaginous disorder; diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT Protein /label= Signal_peptide
 FT Protein 19..197
 FT Protein /label= Mature_IL-17C.polypeptide
 FT Protein /note= "Used to treat degenerative cartilaginous
 disorder"
 FT Misc-difference 109
 FT /note= "Conserved Trp residue"

```
FT Misc-difference 129 /note= "Conserved Cys residue"
FT Misc-difference 134 /note= "Conserved Cys residue"
FT Misc-difference 163 /note= "Conserved Cys residue"
FT Misc-difference 189 /note= "Conserved Cys residue"
FT Misc-difference 191 /note= "Conserved Cys residue"
FT Misc-difference 198.206 /note= "C-terminal Gly(His)8 tag"
XX
XX WO9960127-A2.
XX
XX 25-NOV-1999.
XX
XX 14-MAY-1999; 99WO-US10733.
XX
XX 15-MAY-1998; 98US-0085579.
XX 23-DEC-1998; 98US-0113621.
XX
XX (GETH ) GENENTECH INC.
XX
XX Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WI;
XX
XX WPI; 2000-116314/10.
XX
XX New polypeptides designated PRO1031 and PRO1122 used to treat a
XX degenerative cartilaginous disorder -
XX
XX Example 11; Page 138-139; 141pp; English.
XX
XX The present sequence is the human PRO1122 polypeptide, with a C-terminal
XX Gly(His)8 tag, IL-17C.his, derived from the clone DNA62377-1381-1.
XX This sequence is used in a competitive binding experiment for the
XX immunoprecipitation of IL-17 receptor extracellular domain (IL-17R ECD).
XX The entire coding region of IL-17C can be used as hybridisation probe.
XX The PRO1122 polypeptide, agonist or antagonist, is used to diagnose and
XX treat a degenerative cartilaginous disorder.
XX
XX Sequence 206 AA;

Query Match 100.0%; Score 1073; DB 21; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.9e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLFTWLHTCLAHHDPSLRGPHSHGTPHCYSAAEELPLGOAPPHLLARGAKWGQ 60
Db 1 mtlplgllftwlhtclahhdpslrghphshgtphcysaeelpigqapphllargakwgq 60
QY 61 ALPVALVSSLEAASHRHERPSATTQCPVLRPEEVELEADTHQRSISPWRYRVDTDEDRY 120
Db 61 alpvalvssleaaashrgrherpsattqcpvlrpeevleadthgrsispwryrvdtdedry 120
QY 121 PQKLAFAECLRCGICDARTGRETAAALNSVRLQLSLLVLRRRRCSRDSGLPTPGAFAFHT 180
Db 121 pqklafaeclrcgicdartgretaalnsvrlqlsllvlrrrrpcsrdsrglptpgafafht 180
QY 181 EFTIHPVGCVCVLPVRSV 197
Db 181 eftihpvgctcvlprsv 197

RESULT 11
AAY44462
ID AAY44462 standard; Protein; 425 AA.
XX
XX AAY44462;
XX
XX 27-MAR-2000 (first entry)
XX
```

```
DE Human Interleukin 17C-IgG1 Fc fusion protein, hIL-17C.fc.
XX
XX Interleukin; IL-17C.fc; fusion protein; PRO1122 polypeptide; cytokine;
XX human IgG1; fluorescence-activated cell sorter analysis; FACS;
KW Tumour Necrosis Factor-alpha; TNF-alpha; leukemic monocyte; THP-1 cell.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..18
XX /label= Signal_peptide
XX Protein 19..197
XX /label= Mature_IL-17C-polypeptide
XX /note= "Used to treat degenerative cartilaginous
XX disorder"
XX Misc-difference 109 /note= "Conserved Trp residue"
XX Misc-difference 129 /note= "Conserved Cys residue"
XX Misc-difference 134 /note= "Conserved Cys residue"
XX Misc-difference 163 /note= "Conserved Cys residue"
XX Misc-difference 189 /note= "Conserved Cys residue"
XX Misc-difference 191 /note= "Conserved Cys residue"
XX Region 197..425
XX /note= "Sequence derived from Fc region of human IgG1"
XX
XX WO9960127-A2.
XX
XX 25-NOV-1999.
XX
XX 14-MAY-1999; 99WO-US10733.
XX
XX 15-MAY-1998; 98US-0085579.
XX 23-DEC-1998; 98US-0113621.
XX
XX (GETH ) GENENTECH INC.
XX
XX Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WI;
XX
XX WPI; 2000-116314/10.
XX
XX New polypeptides designated PRO1031 and PRO1122 used to treat a
XX degenerative cartilaginous disorder -
XX
XX Example 12; Page 129-130; 141pp; English.
XX
XX The present sequence is the human IL-17C.fc fusion protein, derived from
XX PRO1122 polypeptide and the Fc region of human IgG1. The cytokine IL-17C
XX can be used to induce the release of TNF-alpha from human leukemic
XX monocytic, THP-1 cells. The fusion protein, IL-17C.fc is used to identify
XX the binding of IL-17C to THP-1 cells, using fluorescence-activated cell
XX sorter analysis (FACS).
XX
XX Sequence 425 AA;

Query Match 100.0%; Score 1073; DB 21; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.3e-108;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLFTWLHTCLAHHDPSLRGPHSHGTPHCYSAAEELPLGOAPPHLLARGAKWGQ 60
Db 1 mtlplgllftwlhtclahhdpslrghphshgtphcysaeelpigqapphllargakwgq 60
QY 61 ALPVALVSSLEAASHRHERPSATTQCPVLRPEEVELEADTHQRSISPWRYRVDTDEDRY 120
Db 61 alpvalvssleaaashrgrherpsattqcpvlrpeevleadthgrsispwryrvdtdedry 120
QY 121 PQKLAFAECLRCGICDARTGRETAAALNSVRLQLSLLVLRRRRCSRDSGLPTPGAFAFHT 180
```

Db 121 pqlkfaecicrgcdartgretaalnsrvllqslvllrrpcsrddsglptpgafahf 180
Qy 181 EFHVPVGCTCVLPKSV 197
Db 181 efihvpvgctcvlpksv 197

RESULT 12
AAE08676
ID AAE08676 standard; Protein; 227 AA.
AC AAE08676;
XX 15-NOV-2001 (first entry)
XX Human interleukin (IL)-17 like protein.
XX Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy;
KW multiple sclerosis; graft versus host disease; inflammatory disease;
KW asthma; autoimmune disease; allergy; graft rejection; bone destruction;
KW drug screening; antiinflammatory; immunosuppressive; antiasthmatic;
KW neuroprotective; antirheumatic; antiallergic.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Peptide 5..48
FT /label= Signal_peptide
FT Protein 49..227
FT /label= Mature_human_IL-17_like protein
XX
XX WO200159120-A2.
XX 16-AUG-2001.
XX 07-FEB-2001; 2001WO-US03916.
XX 08-FEB-2000; 2000US-0180864.
XX 27-NOV-2000; 2000US-0722920.
XX (AMGE-) AMGEN INC.
XX Jing S, Bass MB;
XX WPI; 2001-529841/58.
XX N-PSDB; RAD15291.
XX Novel interleukin-17 like polypeptides and nucleic acid molecules
PT encoding them useful for diagnosis, prevention and treatment of
PT inflammatory, autoimmune disease, allergies, asthma and organ or graft
PT rejection
XX
XX Claim 14; Fig 1A; 117pp; English.

The present invention relates to interleukin (IL)-17 like polypeptides and nucleic acids encoding them. IL-17 like protein is useful for identifying binding partners, agonists and antagonists which can be used for treating one or more diseases or disorders and for cloning IL-17 like receptors, using an expression cloning strategy. Radiolabelled or affinity/activity-tagged IL-17 proteins are useful in binding assays to identify a cell type or cell line or tissue that express IL-17 like receptors. A radiolabelled or tagged IL-17 like protein is useful as an affinity ligand to identify and isolate from an expression library the subset of cells which express the IL-17 like receptors on their surface. IL-17 like protein, agonist and antagonist are useful for treating acute and chronic inflammation such as rheumatic diseases, graft versus host disease and multiple sclerosis. IL-17 like antagonists are useful for treating and preventing inflammatory disease, autoimmune disease, allergies, asthma and organ or graft rejection in a patient and also for inhibiting T cell proliferation and/or activation, in vivo B cell proliferation or immunoglobulin secretion, and for blocking the effects of IL-17 in inducing bone destruction. IL-17 like molecule is useful in

CC gene therapy and for mapping the location of the IL-17 like gene and CC related genes on chromosomes, as hybridisation probes in diagnostic assays. Non-human animals in which the promoter for one or more of IL-17 like protein is either activated or inactivated are useful for drug CC candidate screening. The present sequence is human IL-17 like protein.
XX
SQ Sequence 227 AA;
Query Match 99.1%; Score 1063; DB 22; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.9e-108; Mismatches 0; Indels 0; Gaps 0;
Matches 195; Conservative 0;
Qy 3 LPLGLFLTLTWLHTCLAHDPSSLRGHPHSHGTPTHCYSAEELPLGQAPPHLLARGAKWGQAL 62
Db 33 lllpgllfltlwhtclahdpsslrghphshgtpchysaeelpgqpphllargakwgqal 92
Qy 63 PVALVSSLEAAASHRGHERPSATTCQPVLRPEEVLADTHQRSISPSWRYRVDTDDEDRYPQ 122
Db 93 pvalvssleaaashrgtherpsattgcpvirpeevleadthqrsispwryrvdtdedrypq 152
Qy 123 KLAFACELCRGCDARTGRTAALNSVRLQLSLVLLRRRPGSRDGLPTPGAFAPHTTF 182
Db 153 klafaelcrgcdartgretaalnsrvllqslvllrrpcsrddsglptpgafahf 212
Qy 183 IHVPVGCTCVLPKSV 197
Db 213 ihvpvgctcvlpksv 227

RESULT 13
AAE08680
ID AAE08680 standard; Protein; 227 AA.
XX
AC AAE08680;
XX 15-NOV-2001 (first entry)
XX Human interleukin (IL)-17 like protein mutant (Leu47Ile).
XX Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy;
KW multiple sclerosis; graft versus host disease; inflammatory disease;
KW asthma; autoimmune disease; allergy; graft rejection; bone destruction;
KW drug screening; antiinflammatory; immunosuppressive; antiasthmatic;
KW neuroprotective; antirheumatic; antiallergic; mutant; mutein.
XX Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 47 /note= "Wild-type Leu substituted with Ile"
FT
XX WO200159120-A2.
XX 16-AUG-2001.
XX 07-FEB-2001; 2001WO-US03916.
XX 08-FEB-2000; 2000US-0180864.
XX 27-NOV-2000; 2000US-0722920.
XX (AMGE-) AMGEN INC.
XX Jing S, Bass MB;
XX WPI; 2001-529841/58.
XX Novel interleukin-17 like polypeptides and nucleic acid molecules
PT encoding them useful for diagnosis, prevention and treatment of
PT inflammatory, autoimmune disease, allergies, asthma and organ or graft
PT rejection
XX

PS	Claim 18; Page -: 117pp; English.	XX	
XX	The present invention relates to interleukin (IL)-17 like polypeptides and nucleic acids encoding them. IL-17 like protein is useful for identifying binding partners, agonists and antagonists which can be used for treating one or more diseases or disorders and for cloning IL-17 like receptors, using an expression cloning strategy. Radiolabelled or affinity/activity-tagged IL-17 proteins are useful in binding assays to identify a cell type or cell line or tissue that express IL-17 like receptors. A radiolabelled or tagged IL-17 like protein is useful as an affinity ligand to identify and isolate from an expression library the subset of cells which express the IL-17 like receptors on their surface. IL-17 like protein, agonist and antagonist are useful for treating acute and chronic inflammation such as rheumatic diseases, graft versus host disease and multiple sclerosis. IL-17 like antagonists are useful for treating and preventing inflammatory disease, autoimmune disease, allergies, asthma and organ or graft rejection in a patient and also for inhibiting T cell proliferation and/or activation, in vivo B cell proliferation or immunoglobulin secretion, and for blocking the effects of IL-17 in inducing bone destruction. IL-17 like molecule is useful in gene therapy and for mapping the location of the IL-17 like gene and related genes on chromosomes, as hybridisation probes in diagnostic assays. Non-human animals in which the promoter for one or more of IL-17 like protein is either activated or inactivated are useful for drug candidate screening. The present sequence is human IL-17 like protein mutant (Leu47Ile).	XX	
CC	Note: The present sequence is not shown in the specification, but is derived from the human IL-17 like protein referred to as SEQ ID NO:2 (AAE08676), shown in figure 1A.	CC	
XX	Sequence 227 AA;	XX	
SQ		SQ	
	Query Match 98.9%; Score 1061; DB 22; Length 227; Best Local Similarity 99.5%; Pred. No. 1.1e-107; Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
QY	3 LLPGLLFTWLHTCLAHDPDSLGRPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL 62 	QY	3 LLPGLLFTWLHTCLAHDPDSLGRPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL 62
Db	33 llpgllfltlwtctciiahdpdslgrphshgtpchysaeelpigqapphllargakwgqal 92 	Db	33 llpgllfltlwtctciiahdpdslgrphshgtpchysaeelpigqapphllargakwgqal 92
QY	63 PVALVSSLEAASHRGHERPSATTQCPVLRPPEVLADTHQRSISPWRYRVDDEDRYPQ 122 	QY	63 PVALVSSLEAASHRGHERPSATTQCPVLRPPEVLADTHQRSISPWRYRVDDEDRYPQ 122
Db	93 pvalvsleaashrgtherpsattqcpvirpveevleadthqrsispwryrvdtdedrypq 152 	Db	93 pvalvsleaashrgtherpsattqcpvirpveevleadthqrsispwryrvdtdedrypq 152
QY	123 KLAFAFCLRCGCDIDARTGRETALNSVRLQLSLVLRPPCSRDGSLPTPGAFAPHTF 182 	QY	123 KLAFAFCLRCGCDIDARTGRETALNSVRLQLSLVLRPPCSRDGSLPTPGAFAPHTF 182
Db	153 klafaeclrgcdidartgretaalnsvrlqslvlrrpcsdrgsglptpgafafhtef 212 	Db	153 klafaeclrgcdidartgretaalnsvrlqslvlrrpcsdrgsglptpgafafhtef 212
QY	183 IHVPVGCTCVLPKRSV 197 	QY	183 IHVPVGCTCVLPKRSV 197
Db	213 ihvpvgctcvlprsv 227 	Db	213 ihvpvgctcvlprsv 227
RESULT 14			
AAE08682			
ID	AAE08682 standard; Protein: 227 AA.		
XX			
AC	AAE08682;		
XX			
DT	15-NOV-2001 (first entry)		
XX			
DE	Human interleukin (IL)-17 like protein mutant (Leu47Met).		
XX			
KW	Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy;		
KW	multiple sclerosis; graft versus host disease; inflammatory disease;		
KW	asthma; autoimmune disease; allergy; graft rejection; bone destruction;		
KW	drug screening; antiinflammatory; immunosuppressive; antiasthmatic;		
KW	neuroprotective; antirheumatic; antiallergic; mutant; mutein.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			

FH	Key	Location/Qualifiers	
FT	Misc-difference 47	/note= "Wild-type Leu substituted with Met"	
XX			
PN	WO200159120-A2.		
XX			
PD	16-AUG-2001.		
XX			
PF	07-FEB-2001; 2001WO-US03916.		
XX			
PR	08-FEB-2000; 2000US-0180864.		
PR	27-NOV-2000; 2000US-072920.		
XX			
PA	(AMGE-) AMGEN INC.		
XX			
PI	Jing S, Bass MB;		
XX			
DR	WPI; 2001-529841/58.		
XX			
PT	Novel interleukin-17 like polypeptides and nucleic acid molecules encoding them useful for diagnosis, prevention and treatment of inflammatory, autoimmune disease, allergies, asthma and organ or graft rejection		
PT			
PT			
XX	Claim 18; Page -: 117pp; English.		
XX			
CC	The present invention relates to interleukin (IL)-17 like polypeptides and nucleic acids encoding them. IL-17 like protein is useful for identifying binding partners, agonists and antagonists which can be used for treating one or more diseases or disorders and for cloning IL-17 like receptors, using an expression cloning strategy. Radiolabelled or affinity/activity-tagged IL-17 proteins are useful in binding assays to identify a cell type or cell line or tissue that express IL-17 like receptors. A radiolabelled or tagged IL-17 like protein is useful as an affinity ligand to identify and isolate from an expression library the subset of cells which express the IL-17 like receptors on their surface. IL-17 like protein, agonist and antagonist are useful for treating acute and chronic inflammation such as rheumatic diseases, graft versus host disease and multiple sclerosis. IL-17 like antagonists are useful for treating and preventing inflammatory disease, autoimmune disease, allergies, asthma and organ or graft rejection in a patient and also for inhibiting T cell proliferation and/or activation, in vivo B cell proliferation or immunoglobulin secretion, and for blocking the effects of IL-17 in inducing bone destruction. IL-17 like molecule is useful in gene therapy and for mapping the location of the IL-17 like gene and related genes on chromosomes, as hybridisation probes in diagnostic assays. Non-human animals in which the promoter for one or more of IL-17 like protein is either activated or inactivated are useful for drug candidate screening. The present sequence is human IL-17 like protein mutant (Leu47Met).		
CC	Note: The present sequence is not shown in the specification, but is derived from the human IL-17 like protein referred to as SEQ ID NO:2 (AAE08676), shown in figure 1A.		
XX	Sequence 227 AA;		
SQ			
	Query Match 98.9%; Score 1061; DB 22; Length 227; Best Local Similarity 99.5%; Pred. No. 1.1e-107; Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
QY	3 LLPGLLFTWLHTCLAHDPDSLGRPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL 62 	QY	3 LLPGLLFTWLHTCLAHDPDSLGRPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL 62
Db	33 llpgllfltlwtctciiahdpdslgrphshgtpchysaeelpigqapphllargakwgqal 92 	Db	33 llpgllfltlwtctciiahdpdslgrphshgtpchysaeelpigqapphllargakwgqal 92
QY	63 PVALVSSLEAASHRGHERPSATTQCPVLRPPEVLADTHQRSISPWRYRVDDEDRYPQ 122 	QY	63 PVALVSSLEAASHRGHERPSATTQCPVLRPPEVLADTHQRSISPWRYRVDDEDRYPQ 122
Db	93 pvalvsleaashrgtherpsattqcpvirpveevleadthqrsispwryrvdtdedrypq 152 	Db	93 pvalvsleaashrgtherpsattqcpvirpveevleadthqrsispwryrvdtdedrypq 152
QY	123 KLAFAFCLRCGCDIDARTGRETALNSVRLQLSLVLRPPCSRDGSLPTPGAFAPHTF 182 	QY	123 KLAFAFCLRCGCDIDARTGRETALNSVRLQLSLVLRPPCSRDGSLPTPGAFAPHTF 182
Db	153 klafaeclrgcdidartgretaalnsvrlqslvlrrpcsdrgsglptpgafafhtef 212 	Db	153 klafaeclrgcdidartgretaalnsvrlqslvlrrpcsdrgsglptpgafafhtef 212
QY	183 IHVPVGCTCVLPKRSV 197 	QY	183 IHVPVGCTCVLPKRSV 197
Db	213 ihvpvgctcvlprsv 227 	Db	213 ihvpvgctcvlprsv 227
RESULT 14			
AAE08682			
ID	AAE08682 standard; Protein: 227 AA.		
XX			
AC	AAE08682;		
XX			
DT	15-NOV-2001 (first entry)		
XX			
DE	Human interleukin (IL)-17 like protein mutant (Leu47Met).		
XX			
KW	Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy;		
KW	multiple sclerosis; graft versus host disease; inflammatory disease;		
KW	asthma; autoimmune disease; allergy; graft rejection; bone destruction;		
KW	drug screening; antiinflammatory; immunosuppressive; antiasthmatic;		
KW	neuroprotective; antirheumatic; antiallergic; mutant; mutein.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			

QY 183 IHVPVGCTCVLPKRSV 197
Db 213 ihvpvgctcvlprsv 227

RESULT 15

AAE08681
ID AAE08681 standard; Protein: 227 AA.

XX AAE08681;

DT 15-NOV-2001 (first entry)

XX Human interleukin (IL)-17 like protein mutant (Leu47Val).

XX Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy;
KW multiple sclerosis; graft versus host disease; inflammatory disease;
KW asthma; autoimmune disease; allergy; graft rejection; bone destruction;
KW drug screening; antiinflammatory; immunosuppressive; antiasthmatic;
KW neuroprotective; antirheumatic; antiallergic; mutant; mutein.

XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers

PH Misc-difference 47 /note= "Wild-type Leu substituted with Val"

FT WO200159120-A2.

PN 16-AUG-2001.

XX 07-FEB-2001; 2001WO-US03916.

XX 08-FEB-2000; 2000US-0180864.

PR 27-NOV-2000; 2000US-0722920.

XX (AMGE-) AMGEN INC.

XX Jing S, Bass MB;

XX WPI; 2001-529841/58.

XX Novel interleukin-17 like polypeptides and nucleic acid molecules
PT encoding them useful for diagnosis, prevention and treatment of
PT inflammatory, autoimmune disease, allergies, asthma and organ or graft
PT rejection

PS Claim 18; Page -: 117pp; English.

XX The present invention relates to interleukin (IL)-17 like polypeptides
and nucleic acids encoding them. IL-17 like protein is useful for
identifying binding partners, agonists and antagonists which can be used
for treating one or more diseases or disorders and for cloning IL-17
like receptors, using an expression cloning strategy. Radiolabelled or
affinity/activity-tagged IL-17 proteins are useful in binding assays to
identify a cell type or cell line or tissue that express IL-17 like
receptors. A radiolabelled or tagged IL-17 like protein is useful as an
affinity ligand to identify and isolate from an expression library the
subset of cells which express the IL-17 like receptors on their surface.
IL-17 like protein, agonist and antagonist are useful for treating acute
and chronic inflammation such as rheumatic diseases, graft versus host
disease and multiple sclerosis. IL-17 like antagonists are useful for
treating and preventing inflammatory disease, autoimmune disease,
allergies, asthma and organ or graft rejection in a patient and also
for inhibiting T cell proliferation and/or activation, in vivo B cell
proliferation or immunoglobulin secretion, and for blocking the effects
of IL-17 in inducing bone destruction. IL-17 like molecule is useful in
gene therapy and for mapping the location of the IL-17 like gene and
related genes on chromosomes, as hybridisation probes in diagnostic
assays. Non-human animals in which the promoter for one or more of IL-17
like protein is either activated or inactivated are useful for drug
candidate screening. The present sequence is human IL-17 like

CC protein mutant (Leu47Val).
CC Note: The present sequence is not shown in the specification, but is
CC derived from the human IL-17 like protein referred to as SEQ ID NO:2
CC (AAE08676), shown in figure 1A.

SQ Sequence 227 AA;

Query Match 98.8%; Score 1060; DB 22; Length 227;

Best Local Similarity 99.5%; Pred. No. 1.5e-107;

Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLPGLLFLTWLHTCLAHDPFSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL 62

Db 33 lllpgllfltlwltcvahhdpslrghphshgtphcysaeelpgqapphillargakwgqal 92

QY 63 PVALVSSLEAASHRGHREPSATTCQVLRPEEVLEADTHQRSISPWRYRVDTDEDYPO 122

Db 93 pvalvssleaaashrgtherpsattqcpvirpeevleadthqrsispwryrvdtdedrypq 152

QY 123 KLAFACLCRCGICIDARTGRTAALNSVRLIQSLVLRPPCRSDGSGCLPTPGAFAFHTEF 182

Db 153 klafaelcrgicidartgrettaalnsrvllqslvlrrppcsrdsgslptpgafafhtef 212

QY 183 IHVPVGCTCVLPKRSV 197

Db 213 ihvpvgctcvlprsv 227

Search completed: August 23, 2002, 16:01:48

Job time: 59 sec

Query Match: 100.0%; Score 1073; DB 21; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLFLTWLHTCLAHHDPSLRGPHSHGCTPHCYSAEELPLGQAPPHLLARGAKWQ 60
Db 1 mtclpgllfltlwhtclahhdpslrghshgtpchysaeelpgqapphllargakwq 60
QY 61 ALPVALVSSLEAASHRGHERPSATQCPVLRPEEVLEADTHQSTSPWRYRVDTDEDRY 120
Db 61 alpvalvssleaaashrgherpsattqcpvrpeevleadthqrsispryrvdtdedry 120
QY 121 POKLAFACLCRGCDARTGRTAALNSVRLQSLVLRRCPSRDGSLPTPGAFAPT 180
Db 121 pqklafaelclrgcdartgrettaalnsvrlqlslvrrrrpcsdgsglptpgafafht 180
QY 181 EFHVPVGCCTVLP RSV 197
Db 181 efihvpvgctcvlprsv 197

RESULT 5
RAY44460
ID AAY44460 standard; Protein; 197 AA.
AC AAY44460;
DT 27-MAR-2000 (first entry)
DE Human Interleukin 17C, PRO1122 polypeptide.
KW Interleukin; IL-17C; PRO1122 polypeptide; clone DNA62377-1381-1; UNO561;
KW cytokine IL-17; cytotoxic T-lymphocyte-associated antigen 8; CTLA-8;
KW hybridisation probe; antagonist; degenerative cartilaginous disorder;
KW agonist; diagnosis; therapy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..18
FT Protein /label= Signal_peptide
FT /label= Mature_IL-17C_polypeptide
FT /note= "Used to treat degenerative cartilaginous disorder"
FT Misc-difference 109 /note= "Conserved Trp residue"
FT Misc-difference 129 /note= "Conserved Cys residue"
FT Misc-difference 134 /note= "Conserved Cys residue"
FT Misc-difference 163 /note= "Conserved Cys residue"
FT Misc-difference 189 /note= "Conserved Cys residue"
FT Misc-difference 191 /note= "Conserved Cys residue"
FT /note= "Conserved Cys residue"
XX W09960127-A2.
XX 25-NOV-1999.
XX 14-MAY-1999; 99WO-US10733.
XX 15-MAY-1998; 98US-0085579.
XX 23-DEC-1998; 98US-0113621.
XX (GETH) GENENTECH INC.
XX Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WT;
PI

DR WPI; 2000-116314/10.
XX N-PSDB; AAZ29728.
PT New polypeptides designated PRO1031 and PRO1122 used to treat a
degenerative cartilaginous disorder -
XX Claim 23; Fig 3; 141pp; English.
XX The present sequence is the human PRO1122 polypeptide, also referred to
as UNO561, and as interleukin-17C (IL-17C), encoded by
clone DNA62377-1381-1. This sequence has identity with the
cytokine IL-17 and cytotoxic T-lymphocyte-associated antigen 8 (CTLA-8)
and has leucine zipper pattern. PRO1122 is expressed in pancreas, small
intestine, stomach and testis also. It shares about 26-28% amino acid
identity with IL-17 and IL-17B. The entire coding region of IL-17C can
be used as hybridisation probe. The PRO1122 polypeptide, agonist or
antagonist, is used to diagnose and treat a degenerative cartilaginous
disorder.
XX SQ Sequence 197 AA;
Query Match 100.0%; Score 1073; DB 21; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.6e-109;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLGLLFLTWLHTCLAHHDPSLRGPHSHGCTPHCYSAEELPLGQAPPHLLARGAKWQ 60
Db 1 mtclpgllfltlwhtclahhdpslrghshgtpchysaeelpgqapphllargakwq 60
QY 61 ALPVALVSSLEAASHRGHERPSATQCPVLRPEEVLEADTHQSTSPWRYRVDTDEDRY 120
Db 61 alpvalvssleaaashrgherpsattqcpvrpeevleadthqrsispryrvdtdedry 120
QY 121 POKLAFACLCRGCDARTGRTAALNSVRLQSLVLRRCPSRDGSLPTPGAFAPT 180
Db 121 pqklafaelclrgcdartgrettaalnsvrlqlslvrrrrpcsdgsglptpgafafht 180
QY 181 EFHVPVGCCTVLP RSV 197
Db 181 efihvpvgctcvlprsv 197

RESULT 6
RAY53892
ID AAY53892 standard; Protein; 197 AA.
XX AAY53892;
AC AAY53892;
DT 13-MAR-2000 (first entry)
DE Amino acid sequence of human interleukin-21.
KW Human; interleukin-22; IL-22; IL-21; immune system disorder;
KW immune cell chemotaxis; haematopoietic cell disorder;
KW haemostatic activity; thrombolytic activity; autoimmune disorder; asthma;
KW respiratory problem; organ rejection; graft-versus-host disease; GVHD;
KW inflammation; hyperproliferative disorder; tissue regeneration;
KW embryonic stem cell differentiation; embryonic stem cell proliferation;
KW haematopoietic lineage; allergic asthma.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Peptide 1..18 /note= "signal peptide"
FT Domain 34..40 /note= "conserved domain V"
FT Domain 63..68 /note= "conserved domain VI"
FT Domain 104..109 /note= "conserved domain VII"
FT Domain 113..121

FT Domain /note= "conserved domain I"
 FT 129..134
 FT /note= "conserved domain II"
 FT 156..162
 FT /note= "conserved domain III"
 FT 185..192
 FT /note= "conserved domain IV"
 XX
 PN W09961617-A1.
 XX
 PD 02-DEC-1999.
 XX
 XX 27-MAY-1999; 99WO-US11644.
 XX
 PR 29-MAY-1998; 98US-0087340.
 PR 10-SEP-1998; 98US-009805.
 PR 30-APR-1999; 99US-0131965.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Ebner R;
 XX
 DR WPI: 2000-072622/06.
 DR N-PSDB; AA236836.
 XX
 XX Novel polynucleotides used to develop products for treating e.g. immune disorders, blood disorders, autoimmune disorders, allergies, inflammation, hyperproliferative disorders or infections
 PT
 PT
 PT
 PS Claim 26; Fig 6A-B; 170pp; English.
 XX
 CC The present sequence represents a human interleukin-21 (IL-21) protein. The specification also describes IL-22 polynucleotides and polypeptides. The IL-21 polynucleotide was isolated from a cDNA library of apoptotic T-cells. IL-21 and IL-22 may be useful in treating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells, treating or detecting deficiencies or disorders of haematopoietic cells, to modulate haemostatic or thrombolytic activity, in treating or detecting autoimmune disorders, treating asthma (particularly allergic asthma) or other respiratory problems, to treat and/or prevent organ rejection or graft-versus-host disease (GVHD), to modulate inflammation, to treat or detect hyperproliferative disorders, to treat or detect infectious agents, to differentiate, proliferate and attract cells, leading to the regeneration of tissues. IL-21 and IL-22 may also increase or decrease the differentiation or proliferation of embryonic stem cells and haematopoietic lineage, may be used to modulate mammalian characteristics.
 XX
 SQ Sequence 197 AA;

Query Match 100.08; Score 1073; DB 21; Length 197;
 Best Local Similarity 100.08; Pred. No. 4.6e-109;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTLPLGLFLTWLCLAHDPSPRGHSHCTPHCYSAEELPLGQAPHLILARAKWGQ 60
 Dd 1 mtlplgllfltlwclclahdpsslrghshgtphcysaeelpgqapphlilargakwgq 60
 Qy 61 ALPVALVSSLEAASHRGHERPSATTQCPVLRPEVLEADTHORSISPRVVDDEDY 120
 Dd 61 alpvalvssleashrghersattqcpvrpeevleadthqrsispwryrvdtdedry 120
 Qy 121 POKLAFBCLRGCGIDARTGRTAALNSVRLQSLVLLRRRPPCSRDGSLPTPGAFAPT 180
 Dd 121 pqklafaelcrgcgldartgretaalnsrvllqslvlrrrrpcsdrgsglptpgafafht 180
 Qy 181 EFIHVPVCTCVLPRSV 197
 Dd 181 efihvpvgctcvlprsv 197

RESULT 7
 AAG66121 standard; Protein; 197 AA.
 XX
 AC AAG66121;
 XX
 DT 13-MAR-2002 (first entry)
 XX
 DE Human interleukin (IL)-21 amino acid sequence.
 XX
 KW Interleukin; IL-21; IL-22; immunosuppressive; cytostatic; thrombolytic;
 KW antiinflammatory; antibacterial; gene therapy; human.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT /note= "signal peptide"
 FT Protein 19..197
 FT /note= "mature protein"
 FT Domain 34..40
 FT /note= "conserved domain V"
 FT Domain 63..68
 FT /note= "conserved domain VI"
 FT Domain 104..109
 FT /note= "conserved domain VII"
 FT Domain 113..121
 FT /note= "conserved domain I"
 FT Domain 129..134
 FT /note= "conserved domain II"
 FT Domain 156..162
 FT /note= "conserved domain III"
 FT Domain 185..192
 FT /note= "conserved domain IV"
 XX
 XX US2001023070-A1.
 PD 20-SEP-2001.
 XX
 XX 08-DEC-2000; 2000US-0731816.
 XX
 XX 29-MAY-1998; 98US-087340P.
 XX 30-APR-1999; 98US-131965P.
 XX 09-DEC-1999; 99US-169837P.
 XX 27-MAY-1999; 99US-0320713.
 XX 27-MAY-1999; 99WO-US11644.
 XX
 PA (EBNE/) EBNER R.
 PA (RUBE/) RUBEN S M.
 XX
 PI Ebner R, Ruben SM;
 XX
 DR WPI: 2001-638470/73.
 DR N-PSDB; AA167878.
 XX
 XX New interleukin-21 and interleukin-22 polynucleotides and polypeptides,
 PT useful for treating, preventing or diagnosing e.g. disorders of
 PT hematopoietic cells, autoimmune disorders, or hyperproliferative
 PT diseases
 XX
 PS Claim 26; Fig 6A-B; 87pp; English.
 XX
 CC The invention relates to novel human proteins designated interleukin
 CC (IL)-21 and IL-22. The IL-21 and IL-22 polynucleotides can be used in
 CC linkage analysis as a marker for those specific chromosome, in chromosome
 CC mapping, to control gene expression through triple helix formation or
 CC antisense DNA or RNA, in gene therapy, in identifying individuals from
 CC minute biological samples, as an alternative to restriction fragment
 CC length polymorphism (RFLP) analysis, as polymorphic markers for forensic
 CC purposes, as molecular weight markers, or as diagnostic probes. IL-21 and
 CC IL-22 polypeptides can be used to treat, prevent or diagnose diseases of
 CC the immune system by activating or inhibiting the proliferation,

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OM protein - protein search, using sw model

Run on: August 23, 2002, 16:00:55 ; Search time 26.75 Seconds
(without alignments)
1274.019 Million cell updates/sec

Title: US-09-854-208-3
Perfect score: 1073
Sequence: 1 MTLPLGLFLTLWHTCLAHH.....FHTFHVPGCTCVLPRSV 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1073	100.0	197	4 Q9P0M4	Q9p0m4 homo sapien
2	1065	99.3	197	4 Q9HC75	Q9hc75 homo sapien
3	173	16.1	109	4 Q96P18	Q96p18 homo sapien
4	173	16.1	163	4 Q96PD4	Q96pd4 homo sapien
5	169.5	15.8	180	11 Q99MY3	Q99my3 mus musculus
6	168.5	15.7	180	11 Q9QXT6	Q9qxt6 mus musculus
7	165.5	15.4	177	4 Q9H293	Q9h293 homo sapien
8	160.5	15.0	215	11 Q9CTI4	Q9cti4 mus musculus
9	157.5	14.7	151	12 O40633	O40633 salmeline
10	157.5	14.7	178	11 Q9EQI6	Q9eqi6 mesocricetu
11	157	14.6	141	6 Q95L56	Q95l56 bos taurus
12	154.5	14.4	180	4 Q9UHF5	Q9uhf5 homo sapien
13	136	12.7	78	4 Q9NUE6	Q9nue6 homo sapien
14	129.5	12.1	111	11 Q9EQI7	Q9eqi7 rattus norv
15	110	10.3	148	5 Q19778	Q19778 caenorhabdi
16	95.5	8.9	93	6 Q9BEH5	Q9beh5 equus cabal

17	89.5	8.3	168	2 Q9XDC3	Q9xdc3 herbaspiril
18	89.5	8.3	521	12 Q9DP32	Q9dp32 meleagrid h
19	88.5	8.2	521	12 Q9E1H8	Q9elh8 meleagrid h
20	88	8.2	1548	4 Q9NYW9	Q9nyw9 homo sapien
21	88	8.2	2161	4 Q9Y566	Q9y566 homo sapien
22	86.5	8.1	389	10 Q9LE01	Q9leul arabidopsis
23	86	8.0	297	2 Q99391	Q99391 streptomyce
24	86	8.0	1098	11 Q9JL71	Q9jl71 mus musculu
25	84.5	7.9	317	4 Q9BTV9	Q9btv9 homo sapien
26	84	7.8	179	10 Q93Z24	Q93z24 arabidopsis
27	84	7.8	354	10 Q9SE51	Q9se51 arabidopsis
28	82	7.6	313	3 Q9P795	Q9p795 schizosacch
29	82	7.6	415	10 Q9LG13	Q9lg13 oryza sativ
30	81.5	7.6	306	2 Q9L4D4	Q9l4d4 caenothomas
31	81.5	7.6	380	5 Q9GSZ8	Q9gsz8 caenothabdi
32	81	7.5	553	16 Q9I783	Q9i783 pseudomonas
33	80.5	7.5	283	5 Q9W4E1	Q9w4el drosophila
34	80.5	7.5	358	5 Q9U123	Q9u123 leishmania
35	80.5	7.5	638	4 Q96LD4	Q96ld4 homo sapien
36	80	7.5	408	4 Q96H86	Q96h86 homo sapien
37	80	7.5	411	16 Q86313	Q86313 mycobacteri
38	79.5	7.4	681	5 Q95RM4	Q95rm4 drosophila
39	79.5	7.4	745	13 Q98SJ5	Q98sj5 brachydanio
40	79.5	7.4	1406	5 Q9V4D4	Q9v4d4 drosophila
41	79.5	7.4	1406	5 Q9U1I0	Q9uli0 drosophila
42	79.5	7.4	1408	5 Q9XZU7	Q9xzu7 drosophila
43	79	7.4	465	4 Q9BWD7	Q9bwd7 homo sapien
44	79	7.4	837	4 Q9Y4R8	Q9y4r8 homo sapien
45	79	7.4	837	4 Q9BR21	Q9br21 homo sapien

ALIGNMENTS

RESULT 1

ID	Q9P0M4	PRELIMINARY;	PRT;	197 AA.
AC	Q9P0M4;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	INTERLEUKIN 17C.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20105548; PubMed=10639155;			
RA	Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,			
RA	Gurney A.L., Wood W.I.;			
RT	"Cloning and Characterization of IL-17B and IL17C, Two New Members of			
RT	the IL-17 Cytokine Family";			
RL	Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).			
DR	EMBL; AF152099; AAF28105.1; -.			
SQ	SEQUENCE 197 AA; 21765 MW; BAB0152E18DE7D08 CRC64;			

Query Match 100.0%; Score 1073; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.le-100;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTLLPGLFLTLWHTCLAHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWQ	60
Db	1	MTLLPGLFLTLWHTCLAHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWQ	60
QY	61	ALPVALVSSLEAASHRGHREPSATTCQVLRPEEVEADTHQRSISPWRYRVDTDEDY	120
Db	61	ALPVALVSSLEAASHRGHREPSATTCQVLRPEEVEADTHQRSISPWRYRVDTDEDY	120
QY	121	PKLFAECLRCGCDARTGRTAALNSVRLQLLVLRRCRSDGSGGLTPPGAFPH	180
Db	121	PKLFAECLRCGCDARTGRTAALNSVRLQLLVLRRCRSDGSGGLTPPGAFPH	180

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QY 181 EFTHVPVGCCTVLPVRSV 197
|||||
Db 181 EFTHVPVGCCTVLPVRSV 197

RESULT 2
Q9HC75 ID Q9HC75 PRELIMINARY; PRT; 197 AA.
AC Q9HC75;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE CYTOKINE CX2 PRECUSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang W., He L., Wan T., Yuan Z., Cao X.;
RT "Novel human cytokine CX2 with homology to IL-17.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF142410; AAG27921.1; -.
SQ SEQUENCE 197 AA; 21784 MW; BAFBB49F6314A768 CRC64;

Query Match 99.3%; Score 1065; DB 4; Length 197;
Best Local Similarity 99.5%; Pred. No. 1.3e-99;
Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTLPLGLFLTWLHTCLAHHDPSLRGPHSHGTPHCYSAPELPLGQAPPHLLARGAKWGQ 60
Db 1 MTLPLGLFLTWLHTCLAHHDPSLRGPHSHGTPHCYSAPELPLGQAPPHLLARGAKWGQ 60

QY 61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLADTHORSISPMRYRYVDTDEDY 120
|||||
Db 61 ALPVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLADTHORSISPMRYRYVDTDEDY 120

QY 121 POKLAFACLCRCIDARTGRTAALNSVRLQLSLVLRPPCSRDGSLPTPGAFAFHT 180
Db 121 POKLAFACLCRCIDARTGRTAALNSVRLQLSLVLRPPCSRDGSLPTPGAFAFHT 180

QY 181 EFTHVPVGCCTVLPVRSV 197
|||||
Db 181 EFTHVPVGCCTVLPVRSV 197

RESULT 3
Q96PI8 ID Q96PI8 PRELIMINARY; PRT; 109 AA.
AC Q96PI8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE ML1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21475866; PubMed=11591768;
RA Kawaguchi M., Onuchic L.F., Li X.-D., Essayan D.M., Schroeder J.,
RA Xiao H.-Q., Liu M.C., Krishnaswamy G., Germino G., Huang S.-K.;
RT "Identification of a Novel Cytokine, ML-1, and Its Expression in
RT Subjects with Asthma.";
RL J. Immunol. 167:4430-4435(2001).
DR EMBL; AF332389; AAL14427.1; -.
SQ SEQUENCE 109 AA; 12327 MW; 52C5B34C36DC30EB CRC64;

Query Match 16.1%; Score 173; DB 4; Length 109;
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Best Local Similarity 39.0%; Pred. No. 5.7e-10;
Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

QY 97 LEADTHORSISPMRYRYVDTDEDYPOKLAFAECLRCGCLDARTGRTAALNSVRLQLSL 156
: : ||| ||| | : ||| : : ||| : : ||| : : ||| : : ||| : : |||
Db 16 MSRNIESRSTSPWNVTYTWDPNRYPSEVVOAQCRNLGCINAAQ-GKEDISMNSVPIQOETL 74

QY 157 VLRRR--PCSRDGSGLPTPGAFAFHTEFIHVPVGCCTVLP 194
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 75 VVERKHQGC-----VSFQLEKVLVTVGCTCTVP 103

RESULT 4
Q96PD4 ID Q96PD4 PRELIMINARY; PRT; 163 AA.
AC Q96PD4;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE INTERLEUKIN-17F.
GN IL17F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21475830; PubMed=11591732;
RA Starnes T., Robertson M.J., Sledge G., Kelich S., Nakshatri H.,
RA Broxmeyer H.E., Hromas R.;
RT "Cutting Edge: IL-17F, a novel cytokine selectively expressed in
RT activated T cells and monocytes, regulates angiogenesis and
RT endothelial cell cytokine production.";
RL J. Immunol. 167:4137-4140(2001).
DR EMBL; AF384857; AAK83350.1; -.
SQ SEQUENCE 163 AA; 18045 MW; E5287737C9E7BD46 CRC64;

Query Match 16.1%; Score 173; DB 4; Length 163;
Best Local Similarity 39.0%; Pred. No. 8.9e-10;
Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

QY 97 LEADTHORSISPMRYRYVDTDEDYPOKLAFAECLRCGCLDARTGRTAALNSVRLQLSL 156
: : ||| ||| | : ||| : : ||| : : ||| : : ||| : : ||| : : |||
Db 70 MSRNIESRSTSPWNVTYTWDPNRYPSEVVOAQCRNLGCINAAQ-GKEDISMNSVPIQOETL 128

QY 157 VLRRR--PCSRDGSGLPTPGAFAFHTEFIHVPVGCCTVLP 194
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 129 VVERKHQGC-----VSFQLEKVLVTVGCTCTVP 157

RESULT 5
Q99MY3 ID Q99MY3 PRELIMINARY; PRT; 180 AA.
AC Q99MY3;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CYTOKINE CX1 PRECUSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALEB/C.
RA Zhang W., Cao X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF250308; AAK37427.1; -.
SQ SEQUENCE 180 AA; 20268 MW; AAB4CF5FACA3D11E CRC64;

Query Match 15.8%; Score 169.5; DB 11; Length 180;
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Best Local Similarity 27.0%; Pred. No. 2.2e-09;
Matches 53; Conservative 28; Mismatches 82; Indels 33; Gaps 6;

QY 7 LFLTLWLTCLLA-HHDPSSLRGPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVA 65
DB 7 LFLLLAISIFLAPSPRNTKGRKQGRPS-----PLAPGP-----HOVPLD 48

QY 66 LVSSLEAASHRGHRSPSATTQCPVLRPEEVLAD-----THQRSISPWRYRVDTD 116
DB 49 LVSrvKPYARMEYERNTLGMVAQLRNSSEPAKKCEVNLQLWLSNKRSLSPWGYSLNH 108

QY 117 EDRYPQKLAFAECLRCGIDARTGRTAALNSVRLQSLVLRPCSRDGSGLTPPGAF 176
DB 109 PSRIPADLPPEARCLGCVNPTMOEDRSWVSPVF-SQVPPVRRRLCPQ-----PRPGPC 163

QY 177 AFHTEFIHVPVGCTCV 192
DB 164 RQVVVMEIANGCTCI 179

RESULT 6
Q90XT6 PRELIMINARY; PRT; 180 AA.
AC Q90XT6:
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CYTOKINE-LIKE PROTEIN ZCYT07 (NEURONAL INTERLEUKIN-17 RELATED FACTOR)
DE (INTERLEUKIN 17B).
GN IL17B OR ZCYT07.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
RA Martinez T., Hoffman R., O'Hara P.;
RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE FROM N.A.
RA Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E.,
RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;
RT "Identification of a novel IL-17 related factor: Demonstration of
RT neuronal expression and evaluation as a candidate for the chromosome
RT 5q-linked form of Charcot-Marie-Tooth disease."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184970; AAF01319.1; -
DR EMBL; AF218726; AAG44135.1; -
DR EMBL; BC02271; AAH02271.1; -
DR MGD; MGI:1928397; IL17b.
SQ SEQUENCE 180 AA; 20309 MW; E36F4C72001997C5 CRC64;

Query Match 15.7%; Score 168.5; DB 11; Length 180;
Best Local Similarity 27.0%; Pred. No. 2.8e-09;
Matches 53; Conservative 28; Mismatches 82; Indels 33; Gaps 6;

QY 7 LFLTLWLTCLLA-HHDPSSLRGPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVA 65
DB 7 LFLLLAISIFLAPSPRNTKGRKQGRPS-----PLAPGP-----HOVPLD 48

QY 66 LVSSLEAASHRGHRSPSATTQCPVLRPEEVLAD-----THQRSISPWRYRVDTD 116
DB 49 LVSrvKPYARMEYERNTLGMVAQLRNSSEPAKKCEVNLQLWLSNKRSLSPWGYSLNH 108

QY 117 EDRYPQKLAFAECLRCGIDARTGRTAALNSVRLQSLVLRPCSRDGSGLTPPGAF 176
DB 109 PSRIPADLPPEARCLGCVNPTMOEDRSWVSPVF-SQVPPVRRRLCPQ-----PRPGPC 163
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QY 177 AFHTEFIHVPVGCTCV 192
DB 164 RQVVVMEIANGCTCI 179

RESULT 7
Q9H293 PRELIMINARY; PRT; 177 AA.
AC Q9H293:
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE INTERLEUKIN 17E.
GN IL17E.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125711; PubMed=11058597;
RA Lee J., Ho W.-H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S.,
RA Goddard A.D., Yansura D.G., Vandlen R.L., Wood W.I., Gurney A.L.;
RT "IL-17E, a Novel Proinflammatory Ligand for the IL-17 Receptor Homolog
RT IL-17RH1."
RL J. Biol. Chem. 276:1660-1664(2001).
DR EMBL; AF305200; AAG40848.1; -
SQ SEQUENCE 177 AA; 20330 MW; 52D895710CD59871 CRC64;

Query Match 15.4%; Score 165.5; DB 4; Length 177;
Best Local Similarity 29.7%; Pred. No. 5.5e-09;
Matches 52; Conservative 16; Mismatches 70; Indels 37; Gaps 7;

QY 27 HPHSHTGTHCYS-----AEELPLGQAPPHLLARGAKWGQALPVLSLEAASHRGHR 81
DB 31 HTYSHWSPCCPSKGGDTSEEL-----LRW-STVP---VPPLEPARPNRHPS 73

QY 82 PSATTQCPVLRPEEVLADTHORSISPWRYRVDTDQPKLAFAECLRCGIDARTGR 141
DB 74 CRASEDGP-----NSRAISPMRYELDRDLRLPQDLYHARCCLPCHVSLQTS 122

QY 142 ETAAL-NSVRLQSLVLRPCSRDGSGLTPPGAFATFEIHPVVGCTCVLPR 195
DB 123 HMDPRGNSELLYHNTVFYRRPCHGEGK---THKGYCLERRLYRVSCLACVCVPR 174

RESULT 8
Q9CTI4 PRELIMINARY; PRT; 215 AA.
AC Q9CTI4:
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE 1110006016RIK PROTEIN (FRAGMENT).
GN IL17B OR 1110006016RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yanaka S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
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RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003506; BAB22826.1; -.
DR MGD; MGI:1928997; I117b.
FT NON_TER 1
SQ SEQUENCE 215 AA; 24196 MW; 21468E7E01A92154 CRC64;

Query Match 15.0%; Score 160.5; DB 11; Length 215;
Best Local Similarity 29.8%; Pred. No. 2.2e-08;
Matches 48; Conservative 25; Mismatches 63; Indels 25; Gaps 5;

QY 45 GOAPPHLLARGAKWGQALPVALLVSSLEAASHRGHER-----PSATTQCPVL 91
Db 66 GQRPSFLAPGP---HOVPLDLVSRVKPYARMBEYERNLGEMVAQLRNISEPAKKKCEV- 121
QY 92 RPEVLEADTHQRSISPWRVYRVDTDDEYRQKLAFAECLRCGICDARTGRETAALNSVRL 151
Db 122 ---NLQWLNSKRLSPWGYISNHDPSPRIADLPPEARCLCLGCVNPFMTQEDRSWVSPV 178
QY 152 LQSLVLRRRPCRDGSLPTPGAFAFHTEFIHVPVGCCTV 192
Db 179 F-SQVPRRLCPQP----PRPGPCRQVRVVMETIAGVCTCI 214

RESULT 9
Q040633 PRELIMINARY; PRT; 151 AA.
AC O40633;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERLEUKIN 17.
GN ORF13.
OS Saimiriine herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-488;
RX MEDLINE=98037620; PubMed=9371569;
RA Knappe A., Hiller C., Thurnau M., Wittmann S., Hofmann H.,
RA Fleckenstein B., Fickenscher H.;
RT "The superantigen-homologous viral immediate-early gene iel4/vsag in
herpesvirus saimiri-transformed human T cells.";
RL J. Virol. 71:9124-9133(1997).
DR EMBL; Y13183; CAAT3627.1; -.
SQ SEQUENCE 151 AA; 17189 MW; 49B2C9430C46BE32 CRC64;

Query Match 14.7%; Score 157.5; DB 12; Length 151;
Best Local Similarity 28.6%; Pred. No. 3e-08;
Matches 46; Conservative 22; Mismatches 58; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHLLARGAKWGQALPVALLVSSLEAASHRGHERPSATTQCPVLRPEE 95
Db 18 CIVKSEITSATQPRCLAA-----NNSFPRSVVMVLTIRNWTSSKKRAS----- 60
QY 96 VLEADTHQRSISPWRVYRVDTDDEYRQKLAFAECLRCGICDARTGRETAALNSVRLQSL 155
Db 61 ----DYNNRSTSPWTLRYRNDQDRYPSVIWEAKRYLGCVNA-DGNVDYHMNSVPIQOEI 115
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QY 156 LVLR--RPCRSDGSLPTPGAFAFHTEFIHVPVGCCTVLP 194
Db 116 LVVRKGNPCPN-----SFRLEKMLVTVGCTCVTP 145

RESULT 10
Q9EQI6 PRELIMINARY; PRT; 178 AA.
AC Q9EQI6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE NEURONAL INTERLEUKIN-17 RELATED FACTOR (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E.,
RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;
RT "Identification of a novel IL-17 related factor: Demonstration of
neutrophil expression and evaluation as a candidate for the chromosome
5q-linked form of Charcot-Marie-Tooth disease.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF218725; AAG44134.1; -.
FT NON_TER 178
SQ SEQUENCE 178 AA; 20071 MW; 03D02D60BEC89A51 CRC64;

Query Match 14.7%; Score 157.5; DB 11; Length 178;
Best Local Similarity 29.5%; Pred. No. 3.6e-08;
Matches 46; Conservative 23; Mismatches 70; Indels 17; Gaps 4;

QY 45 GOAPPHLLARGAKWGQALPVALLVSSLEAASHRGHERPSATTQCPVLRPEVLEAD---- 100
Db 31 GOVRPGFLAPGP---HQVPLDLVSRVKPYARMBEYERNLGEMVAQLRNSEPAKRRCEVN 87
QY 101 ----THORSISPWRVYRVDTDDEYRQKLAFAECLRCGICDARTGRETAALNSVRLQSL 155
Db 88 LQLWLSNKRSLSPWGYISNHDPSPRIADLPPEARCLCLGCVNPFMTQEDRSWVSPV-SQ 146
QY 156 LVLR--RPCRSDGSLPTPGAFAFHTEFIHVPVGCCTC 191
Db 147 VVVRRLCPQP----PRPGPCRHRVVMETIAGVCTC 178

RESULT 11
Q95L56 PRELIMINARY; PRT; 141 AA.
AC Q95L56;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERLEUKIN 17 (FRAGMENT).
GN IL17.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee I.-K., Mwangi S.M., Olsen S., Kehrli M. Jr.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416586; AAL08013.1; -.
FT NON_TER 1
FT CHAIN 11 141 INTERLEUKIN 17.
SQ SEQUENCE 141 AA; 15945 MW; 94077A79DD803F3E CRC64;

Query Match 14.6%; Score 157; DB 6; Length 141;
```

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SQ      SEQUENCE      180 AA; 20437 MW;  F1B0BC1446D0B14A  CRC64;

Query Match      14.4%; Score 154.5; DB 4; Length 180;
Best Local Similarity 28.7%; Pred. No. 7.3e-08;
Matches 45; Conservative 25; Mismatches 70; Indels 17; Gaps 4;

QY      45  GOAPPHLLARGAKWGQALPVALVSSLEAASHRGRHERPSATTQCPVLRPEVLEAD--- 100
Db      11  | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
31  GCGRPGPLGPGP---HQVPLDLVSRMKPYARMEEYERNTEEMVAQLRNSSELAQRKCEVN 87
QY      101 -----THQSIISPRYRVDTDEDRYQKLAFAECLRGCGIDARTGRTAALNSVRLQLSL 155
Db      : : : | | | | | : | | | | | : | | | | | : | | | | | :
88  LQLWMSNKRSLSPWGYSIINHPSRIEVDLPEARCLGLGCVNPFTMQEDRSWVSPVF-SQ 146
QY      156  LVLRNRRPSRSGSLPTPGAFAPHTFEFIHVPVGCTCV 192
Db      : : | | | | | : | | | | | : | | | | | : | | | | | :
147  VPVRRRLCPPP-----PRTGFCRORAVMETIANGCTCI 179

RESULT 13
Q9NUE6 PRELIMINARY; PRT; 78 AA.
ID Q9NUE6 PRELIMINARY; PRT; 78 AA.
AC Q9NUE6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE DJ108C2.3 (PUTATIVE NOVEL PROTEIN SIMILAR TO IL17 (INTERLEUKIN 17
DE (CYTOTOXIC T-LYMPHOCTE-ASSOCIATED SERINE ESTERASE 8)) (CYTOTOXIC T
DE LYMPHOCTE-ASSOCIATED ANTIGEN 8, CTLA8)) (FRAGMENT).
DE DJ108C2.3.
GN Homo sapiens (Human).
OS
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Almeida J.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL034343; CAB75300.1; -.
DR NON_TER 1
SQ      SEQUENCE      78 AA; 8704 MW;  66C3C34E7ACC2790  CRC64;

Query Match      12.7%; Score 136; DB 4; Length 78;
Best Local Similarity 39.3%; Pred. No. 2.1e-06;
Matches 33; Conservative 14; Mismatches 23; Indels 14; Gaps 3;

QY      113  VDTDEDRYQKLAFAECLRGCGIDARTGRTAALNSVRLQLSLVLRRR--PCSRDGSGL 170
Db      1  | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
1  VTWDPNRYSEVVVQAQCRNLGCINAQ-GREDISMNSVPQQETLVYVRKHGQCS----- 53
QY      171  PTFGAPAFHTFEIHVPVGCTCVLP 194
Db      : | | | | | : | | | | | : | | | | | : | | | | | :
54  -----VSFOLEKVLVTVGCTCTVP 72

RESULT 14
Q9EQI7 PRELIMINARY; PRT; 111 AA.
ID Q9EQI7 PRELIMINARY; PRT; 111 AA.
AC Q9EQI7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE NERF (FRAGMENT).
DE Rattus norvegicus (Rat).
OS
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E.,
RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;

```

RT "Identification of a novel IL-17 related factor: Demonstration of
RT neuronal expression and evaluation as a candidate for the chromosome
RT 5q-linked form of Charcot-Marie-Tooth disease."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF218724; AAG44133.1; -

FT NON_TER 1 1

FT NON_TER 111 111

SQ SEQUENCE 111 AA; 12628 MW; D1598992981BA867 CRC64;

Query Match 12.1%; Score 129.5; DB 11; Length 111;
Best Local Similarity 37.8%; Pred. No. 1.4e-05;
Matches 28; Conservative 16; Mismatches 25; Indels 5; Gaps 2;

QY 101 THORISPMRYRVDTDEDYPOKLAFAECLRCGCDARTGRTAALNSVRLQLSLVLR 160

Db ::::||||| : : : | : | | | | : : | : : | : : | : : | : : | : : |

30 SNKRSLSPMGYSTINHPDRIPEDLPARCLCLGCVNPFTMQEDRSMSVVPF-SQVPVRR 88

QY 161 RPCSRDGSGLPTPG 174

Db | : : | : |

89 RLCPOP-PRPG 98

RESULT 15

Q19778

ID Q19778 PRELIMINARY; PRT; 148 AA.

AC Q19778;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE F25D1.3 PROTEIN.

GN F25D1.3.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RA Kelly P.F.;

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99069613; Pubmed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for

RT investigating biology.";

RL Science 282:2012-2018(1998).

DR EMBL: Z73973; CAA98268.1; -

SQ SEQUENCE 148 AA; 16738 MW; ADB51F438DFB3940 CRC64;

Query Match 10.3%; Score 110; DB 5; Length 148;
Best Local Similarity 33.0%; Pred. No. 0.0018;
Matches 31; Conservative 17; Mismatches 34; Indels 12; Gaps 4;

QY 103 QRSISPMRYRVDTDEDYPOKLAFAECLRCGCDARTGRTAALNSVRLQLSLVLR 162

Db ::::||||| : : : | : | | | | : : | : : | : : | : : | : : |

51 ERALCPWDSRVNYQESREPKLIAESVCLC-----RKSRGSTGAFCMPIVRKVPILRRVS 104

QY 163 CSRDGSLPTPGAFATHTFEIHVPVCTCVLP 196

Db | : : | : | : | : | : | : | : | : | : | : | : |

105 CDR-STGL---WNVVRSTELI--TVGCHSVLPRT 132

Search completed: August 23, 2002, 16:03:07
Job time: 132 sec


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Db 1 MTLPLGLLELFWLHTCLAHDPSSLRGLPHSHGTPHCYSABELPLGQAPHLARGAKWGQ 60
QY 61 ALPVALVSSLEAAASHRGRPSATTCQVLRPEEVELEADTHORSISPMRYRVDTDDEY 120
Db 61 ALPVALVSSLEAAASHRGRPSATTCQVLRPEEVELEADTHORSISPMRYRVDTDDEY 120
QY 121 POKLAFACLCRCIDARTGRTAALNSVRLQSLVLRRLRRPCSRDGSGLPTPGAFAFHT 180
Db 121 POKLAFACLCRCIDARTGRTAALNSVRLQSLVLRRLRRPCSRDGSGLPTPGAFAFHT 180
QY 181 EFTHPVPGCTCVLPVRSV 197
Db 181 EFTHPVPGCTCVLPVRSV 197

RESULT 2
IL17F_HUMAN STANDARD; PRT; 153 AA.
ID IL17F_HUMAN Q96PD4; Q9NUE6; Q96PI8;
AC Q96PD4; Q9NUE6; Q96PI8;
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE Interleukin-17F precursor (IL-17F) (Interleukin-24) (Cytokine ML-1).
GN IL17F OR IL24.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21475830; PubMed=11591732;
RA Starnes T., Robertson M.J., Sledge G., Kelich S., Nakshatri H.,
RA Broxmeyer H.E., Hromas R.;
RT "IL-17F, a novel cytokine selectively expressed in activated T cells
RT and monocytes, regulates angiogenesis and endothelial cell cytokine
RT production.";
RL J. Immunol. 167:4137-4140(2001).
RN [2]
RP SEQUENCE OF 2-153 FROM N.A.
RX MEDLINE=21475866; PubMed=11591768;
RA Kawaguchi M., Onuchic L.F., Li X.-D., Essayan D.M., Schroeder J.,
RA Xiao H.-Q., Liu M.C., Krishnaswamy G., Germino G., Huang S.-K.;
RT "Identification of a novel cytokine, ML-1, and its expression in
RT subjects with asthma.";
RL J. Immunol. 167:4430-4435(2001).
RN [3]
RP SEQUENCE OF 76-153 FROM N.A.
RA Almeida J.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RX X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS), AND CHARACTERIZATION.
RP PubMed=11574464;
RA Hymowitz S.G., Filvaroff E.H., Yin J.P., Lee J., Cai L., Risser P.,
RA Maruoka M., Mao W., Foster J., Kelley R.F., Pan G., Gurney A.L.,
RA de Vos A.M., Starovasinik M.A.;
RT "IL-17s adopt a cysteine knot fold: structure and activity of a novel
RT cytokine, IL-17F, and implications for receptor binding.";
RL EMBO J. 20:5332-5341(2001).
CC -!- FUNCTION: Stimulates the production of other cytokines such as IL-
CC 6, IL-8 and granulocyte colony-stimulating factor, and can
CC regulate cartilage matrix turnover. Stimulates PBMC and T-cell
CC proliferation. Inhibits angiogenesis.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in activated, but not resting, CD4+
CC T cells and activated monocytes.
CC -!- SIMILARITY: BELONGS TO THE IL-17 FAMILY.

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CC -----
CC EMBL; AF384857; AAK83350.1; ALT INIT.
DR EMBL; AF332389; AAL14427.1; ALT_INIT.
DR EMBL; AL034343; CAB75300.1; -.
DR MIM; 606496; -.
DR PDB; 1JPY; 28-SEP-01.
KW Cytokine; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 153 INTERLEUKIN-17F.
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .).
FT DISULFID 37 37 INTERCHAIN (WITH C-127').
FT DISULFID 92 142
FT DISULFID 97 144
FT DISULFID 127 127 INTERCHAIN (WITH C-37').
SQ SEQUENCE 153 AA; 17009 MW; BB489BED863D57CE CRC64;

Query Match 16.1%; Score 173; DB 1; Length 153;
Best Local Similarity 39.0%; Pred. No. 1.7e-09;
Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

QY 97 LEADTHORSISPMRYRVDTDDEYPOKLAFAECLRCGCDARTGRTAALNSVRLQSL 156
Db 60 MSRNIESRSTSPWNTVTWDPNRPSEVQAQCRNLGCINAAQ-GKEDISMNSVPIQOETL 118
QY 157 VLRRR--PCSRDGSGLPTPGAFAFHTFTHVPVGCCTVLP 194
Db 119 VVRKHQGC-----VSFQLEKVLVTGCTCVTP 147

RESULT 3
IL17B_MOUSE STANDARD; PRT; 180 AA.
ID IL17B_MOUSE Q9QXT6; Q99MY3; Q9CTI4;
AC Q9QXT6; Q99MY3; Q9CTI4;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-17B precursor (IL-17B) (Cytokine-like protein ZCYTO7)
DE (Neuronal interleukin-17 related factor) (Cytokine CX1).
GN IL17B OR ZCYTO7 OR N1RF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
RA Martinez T., Hoffman R., O'Hara P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E.,
RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;
RT "Identification of a novel IL-17 related factor: demonstration of
RT neuronal expression and evaluation as a candidate for the chromosome
RT 5q-linked form of Charcot-Marie-Tooth disease.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Zhang W., Cao X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
```

RESULT	4
ID	IL17E_HUMAN
AC	Q9H293;
DT	01-MAR-2002 (Rel. 41, Created)
DT	01-MAR-2002 (Rel. 41, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)
DE	Interleukin-17E precursor (IL-17E).
GN	IL17E.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21125711; PubMed=11058597;
RA	Lee J., Ho W.-H., Marucka M., Corpuz R.T., Baldwin D.T., Foster J.S.,
RA	Goddard A.D., Yansura D.G., Vandlen R.L., Wood W.I., Gurney A.L.;
RT	"IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog
RT	IL-17Rhl.";
RL	J. Biol. Chem. 276:1660-1664 (2001).
CC	-!- FUNCTION: Induces activation of NF-kappaB and stimulates
CC	production of the proinflammatory chemokine IL-8.
CC	-!- SUBCELLULAR LOCATION: Secreted.
CC	-!- TISSUE SPECIFICITY: Expressed at low levels in several tissues,
CC	including brain, kidney, lung, prostate, testis, spinal cord,
CC	adrenal gland, and trachea.
CC	-!- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL: AF305200; ANG40848.1; -
DR	MIW; 605658; -
KW	Cytokine; Glycoprotein; Signal.
FT	SIGNAL
FT	CHAIN 1 32 POTENTIAL.
FT	DISULFID 110 168 INTERLEUKIN-17E.
FT	DISULFID 115 170 BY SIMILARITY.
FT	CARBOHYD 136 136 BY SIMILARITY.
FT	N-LINKED (GLCNAC...) (POTENTIAL).
SQ	SEQUENCE 177 AA; 20330 MW; 52D895710CD59871 CRC64;
Query Match	15.4%; Score 165.5; DB 1; Length 177;
Best Local Similarity	29.7%; Pred.No. 1e-08;
Matches	52; Conservative 16; Mismatches 70; Indels 37; Gaps 7;
QY	27 HPISHGTHPHCYSD----AEELPLGQAPHLHARGAKWGQALPVALSSEAAASHRGHER 81
Db	: : : : : : : : : : : : :
Db	31 HTYSHWSPCCPSKGODTFSEEL-----LRW-STVP---VPPLEPARPNRHPS 73
QY	82 PSATTQCPLVRPEVLVDADTHORSIPRRVTDDEDPYOKLAFAECLRCGCIDATGR 141
Db	: :
Db	74 CRASEDGPL-----NSRAISPWRVELDRDLNRPLPDQLYHARCCLPGHCVSLOTGS 122
QY	142 ETAAL-NSVRLLOSLVLRPRPCSRDGSGLPPTGCAFAFHTEFHPVGCTCVLPR 195
Db	:: ::
Db	123 HM DPRGNSELNYNQTVFYRRPCHGEK-----THKGYCLERRLYRVSLACVCVRRP 174
RESULT	5
ID	VG13_HSUSA
AC	P24916;
DT	01-MAR-1992 (Rel. 21, Created)
DT	01-MAR-1992 (Rel. 21, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)

RESULT	6			
ID	IL17_HUMAN	STANDARD;	PRT;	155 AA.
AC	Q16552;			
DC	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DI	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-17 precursor (IL-17) (IL-17A) (Cytotoxic T lymphocyte-associated antigen 8) (CTLA-8).			
DN	IL17 OR IL17A OR CTLA8.			
GE	Homo sapiens (Human)			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=96281911; PubMed=8676080;			
RX	Fossiez F., Djossou O., Chomarat P., Flores-Romo L., Ait-Yahia S., Maat C., Pin J.-J., Garrone P., Garcia E., Saeland S., Blanchard D., Gaillard C., Das Mahapatra B., Rouvier E., Golstein P., Bauchereau J., Lebecque S.;			
RT	"T cell interleukin-17 induces stromal cells to produce proinflammatory and hematopoietic cytokines.";			
FT	J. Exp. Med. 183:2593-2603(1996).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=T-cell;			
RC	MEDLINE=96094436; PubMed=7499828;			
RX	Yao Z., Painter S.L., Fanslow W.C., Ulrich D., Macduff B.M., Spriggs M.K., Armitage R.J.;			
RA	"Human IL-17: a novel cytokine derived from T cells.";			
RL	J. Immunol. 155:5483-5486(1995).			
CC	-I- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND HEMATOPOIETIC CYTOKINES. ENHANCES THE SURFACE EXPRESSION OF THE INTRACELLULAR ADHESION MOLECULE-1 (ICAM-1) IN FIBROBLASTS.			
CC	-I- SUBUNIT: HOMODIMER.			
CC	-I- SUBCELLULAR LOCATION: Secreted.			
CC	-I- TISSUE SPECIFICITY: RESTRICTED TO ACTIVATED MEMORY T-CELLS.			
CC	-I- PTM: FOUND BOTH IN GLYCOSYLATED AND NONGLYCOSYLATED FORMS.			
CC	-I- SIMILARITY: BELONGS TO THE IL-17 FAMILY.			
CC	-I- DATABASE: NAME=R&D Systems' cytokine mini-reviews: IL17; WWW='http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=211'.			
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DR	EMBL; Z58820; CAA91233.1; --			
DR	EMBL; U32659; AAC50341.1; --			
DR	MTM; 603149; --			
KW	Cytokine; Glycoprotein; T-cell; Antigen; Signal.			
FT	SIGNAL 1 23 POTENTIAL.			
FT	CHAIN 24 155 INTERLEUKIN-17.			
FT	DISULFID 94 144 BY SIMILARITY.			
FT	DISULFID 99 146 BY SIMILARITY.			
FT	CARBOHYD 68 68 N-LINKED (GLCNAC...) (POTENTIAL).			
SQ	SEQUENCE 155 AA; 17504 MW; 2BCAB9CB2F4886D1 CRC64;			
	Query Match 14.7%; Score 158; DB 1; Length 155;			
	Best Local Similarity 39.8%; Pred. No. 4.5e-08;			
	Matches 39; Conservative 11; Mismatches 34; Indels 14; Gaps 3;			
QY	99 ADTHORSISPRWYRDVEDRYPOKFAECLRGCIDARTGRETAAINSVRLQLSLVL 158 : : : : : : :			
Db	64 SDYNRSTSPWNLRNEDPERPSVIWEAKCRHLGCINA-DGNVDYHMNSVP IQEILVL 122 : : :			
QY	159 RRRP--CSRDSGSGUPTPGAFHTFEFHVPVCPLP 194 : : :			

Db 123 RREPPHCPN-----SFRLEKILVSGCTCVTP 149

RESULT 7

VG13_HSVSC
ID VG13_HSVSC STANDARD; PRT; 151 AA.
AC O40633;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE Immediate early gene 13 protein precursor.
GN 13.
OS Herpesvirus saimiri (subgroup C / strain 488).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10384;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98037620; PubMed=9371569;
RA Knappe A., Hiller C., Thureau M., Wittmann S., Hofmann H.,
RA Fleckenstein B., Fickenscher H.;
RT "The superantigen-homologous viral immediate-early gene iel4/vsag in
RT herpesvirus saimiri-transformed human T cells.";
RL J. Virol. 71:9124-9133(1997).
CC
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-17 FAMILY.

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EMBL: Y13183; CAA73627.1; -

KW Cytokine; Early protein; Signal.

FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 151 IMMEDIATE EARLY GENE 13 PROTEIN.
FT DISULFID 90 140 BY SIMILARITY.
FT DISULFID 95 142 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 151 AA; 17189 MW; 49B2C9430C46BE32 CRC64;

Query Match 14.7%; Score 157.5; DB 1; Length 151;

Best Local Similarity 28.6%; Pred. No. 4.9e-08;

Matches 46; Conservative 22; Mismatches 58; Indels 35; Gaps 5;

Qy 36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAAASHRGHRHPSATTQCPVLRPEE 95
Db 18 CLIVKSEIISAQTPRCLAA-----NNSFPRSVNVLTSIRNWTSSRRAS----- 60

Qy 96 VLEADTHORSISPWRYRVDTDREYPQKLAFAECLRCGICDARTGRTAALNSVRLQSL 155

Db 61 ----DYNNRSTSPWLYRNEQDQRYPSVTWEAKRYLGCVNA-DGNVDYHMNSVPIQOEI 115

Qy 156 LVLR--RPSRDGSLPTPGAFHTEFIHVPVGTCTVLP 194

Db 116 LVVRKGHNPCPN-----SFRLEKMLTVGTCVTP 145

RESULT 8

IL17B_MESAU

ID IL17B_MESAU STANDARD; PRT; 178 AA.

AC Q9EQI6;

DT 01-MAR-2002 (Rel. 41, Created)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DE Interleukin-17B precursor (IL-17B) (Neuronal interleukin-17 related

factor) (Fragment).

GN IL17B OR N1RF.

OS Mesocricetus auratus (Golden hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

OC Mesocricetus.

OX NCBI_TaxID=10036;

RN [1]

RP SEQUENCE FROM N.A.

RA Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E.,

RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;

RT "Identification of a novel IL-17 related factor: demonstration of

RT neuronal expression and evaluation as a candidate for the chromosome

RT Sq-linked form of Charcot-Marie-Tooth disease.";

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Stimulates the release of tumor necrosis factor alpha

CC and IL-beta from the monocytic cell line THP-1 (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE IL-17 FAMILY.

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CC or send an email to license@isb-sib.ch).

EMBL: AF218725; AAG44134.1; -

KW Cytokine; Glycoprotein; Signal.

FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 >178 INTERLEUKIN-17B.

FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DISULFID 121 176 BY SIMILARITY.

FT DISULFID 126 178 BY SIMILARITY.

FT NON_TER 178 178

SQ SEQUENCE 178 AA; 20071 MW; 03D02D60BEC89A51 CRC64;

Query Match 14.7%; Score 157.5; DB 1; Length 178;

Best Local Similarity 29.5%; Pred. No. 5.9e-08;

Matches 46; Conservative 23; Mismatches 70; Indels 17; Gaps 4;

Qy 45 GQAPPHLLARGAKWGQALPVALVSSLEAAASHRGHRHPSATTQCPVLRPEEVLAD---- 100
Db 31 GQVRPGPLAGP---HQVPLDLVSRVKPYARMEEYERNLGMVAQLRNSSEPAKRCEVN 87

Qy 101 -----THORSISPWRYRVDTDREYPQKLAFAECLRCGICDARTGRTAALNSVRLQSL 155

Db 88 LQLWLSNKRSLSPWGYISINHDPSRIPADLPFARCLCLGCVNFTMQEDRSVMVSPVF-SQ 146

Qy 156 LVLR--RPSRDGSLPTPGAFHTEFIHVPVGTCTC 191

Db 147 VVRRRLCPPP-----PRGPRHRVVMETIAGVCTC 178

RESULT 9

IL17B_HUMAN

ID IL17B_HUMAN STANDARD; PRT; 180 AA.

AC Q9UHF5;

DT 01-MAR-2002 (Rel. 41, Created)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DE Interleukin-17B precursor (IL-17B) (Cytokine-like protein zcyt07)

DE (Neuronal interleukin-17 related factor) (interleukin-20).

GN IL17B OR ZCYT07 OR N1RF OR IL20.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,

RA Martinez T., Hoffman R., O'Hara P.;

CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	RL	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC	-----	CC	-!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS THE CONSENSUS SEQUENCE
CC	-----	CC	5'-DHMTATTGATTTWMD-3' ON A VARIETY OF GENE PROMOTERS SUCH AS THOSE
DR	EMBL; AF035581; AAD02033.1; -.	CC	OF HNF3B AND TTR. IMPORTANT FOR LIVER GENES TRANSCRIPTION (BY
DR	EMBL; AF035580; AAD02033.1; JOINED.	CC	SIMILARITY).
DR	EMBL; U96173; AAD00826.1; -.	CC	-!- SUBUNIT: BINDS DNA AS A MONOMER (BY SIMILARITY).
DR	EMBL; Y17739; CAB50769.1; -.	CC	-!- SUBCELLULAR LOCATION: Nuclear.
DR	EMBL; U77975; AAB61705.1; -.	CC	-!- SIMILARITY: CONTAINS 1 CUT DOMAIN.
DR	TRANSFAC; T03286; -.	CC	-!- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEBOX PROTEINS.
DR	MIM; 604164; -.	CC	-----
DR	InterPro; IPR003350; CUT.	CC	This SWISS-PROT entry is copyright. It is produced through a collabor
DR	InterPro; IPR001356; Homeobox.	CC	between the Swiss Institute of Bioinformatics and the EMBL outstat
DR	Pfam; PF023376; CUT; 1.	CC	the European Bioinformatics Institute. There are no restrictions on
DR	Pfam; PF000046; homeobox; 1.	CC	use by non-profit institutions as long as its content is, in no
DR	SMART; SM00389; HOX; 1.	CC	modified and this statement is not removed. Usage by and for comm
DR	PROSITE; PS00027; HOMEBOX_1; FALSE_NEG.	CC	entities requires a license agreement (See http://www.isb-sib.ch/anno
DR	PROSITE; PS00071; HOMEBOX_2; 1.	CC	or send an email to license@isb-sib.ch)

CC	EMBL; U95945; AAB53863.1; -.
DR	TRANSFAC; T03296; -.
DR	MGI; MGI:1196423; Onecut1.
DR	InterPro: IPR003350; CUT.
DR	InterPro: IPR001356; Homeobox.
DR	Pfam; PF02376; CUT; 1.
DR	Pfam; PF00046; homeobox; 1.
DR	SMART; SM00389; HOX; 1.
DR	PROSITE; PS00027; HOMEBOX_1; FALSE_NEG.
DR	PROSITE; PS00071; HOMEBOX_2; 1.
DR	Transcription regulation; Homeobox; DNA-binding; Nuclear protein;
KW	Activator.
FT	DNA_BIND 283 369 CUT.
FT	DNA_BIND 385 444 HOMEBOX.
FT	DOMAIN 69 72 POLY-HIS.
FT	DOMAIN 124 138 POLY-HIS.
FT	DOMAIN 455 460 POLY-SER.
FT	VARIANT 75 75 P -> A.
FT	/FTID-VAR_010729.
FT	A -> T (IN REF. 3 AND 4).
FT	S -> N (IN REF. 4).
FT	Q -> H (IN REF. 4).
FT	R -> K (IN REF. 4).
FT	K -> Q (IN REF. 4).
FT	SEQUENCE 465 AA; 51023 MW; F47F78957A6ECFC2 CRC64;
SQ	
Query Match	8.0%; Score 85.5; DB 1; Length 465;
Best Local Similarity	25.8%; Pred. No. 1;

[illegible]

QY	160	KRPCKR	185
DB	367	LAACKR	372
RESULT 13			
HNF6_MOUSE		STANDARD;	PRT; 465 AA.
ID	HNF6_MOUSE		
AC	O08755;		
DT	16-OCT-2001 (Rel. 40, Created)		
DD	16-OCT-2001 (Rel. 40, Last sequence update)		
DE	16-OCT-2001 (Rel. 40, Last annotation update)		
DEF	Hepatocyte nuclear factor 6 (HNF-6) (One cut domain family member 1).		
DG	ONECUT1 OR HNF6A OR HNF6.		
GN	Mus musculus (Mouse)		
OS	Mus musculus (Mouse)		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RP	TISSUE=Liver;		
RA	Samadani U., Rausa F., Costa R.H.;		
RT	*Mouse hepatocyte nuclear factor-6 cDNA.*;		
RESULT 14			
HNF6_RAT		STANDARD;	PRT; 465 AA.
ID	HNF6_RAT		
AC	P70512; O08755;		
DT	16-OCT-2001 (Rel. 40, Created)		
DD	16-OCT-2001 (Rel. 40, Last sequence update)		
DE	16-OCT-2001 (Rel. 40, Last annotation update)		
DEF	Hepatocyte nuclear factor 6 (HNF-6) (One cut domain family member 1).		
DG	ONECUT1 OR HNF6A OR HNF6.		
GN	Rattus norvegicus (Rat).		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		

RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RM MEDLINE=96382488; PubMed=8790352;
RA Lemaigre F.P., Durvieux S.M., Truong O., Lannoy V.J., Hsuan J.J.,
R Rousseau G.G.;
RT "Hepatocyte nuclear factor 6, a transcription factor that contains a
RL novel type of homeodomain and a single cut domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:9460-9464(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=Wistar;
RX MEDLINE=98256275; PubMed=9593691;
RA Lannoy V.J., Buerklin T.R., Rousseau G.G., Lemaigre F.P.;
RT "Isoforms of hepatocyte nuclear factor-6 differ in DNA-binding
RT properties, contain a bifunctional homeodomain, and define the new
RT ONECUT class of homeodomain proteins.";
RL J. Biol. Chem. 273:13552-13562(1998).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=97042457; PubMed=8887657;
RA Samadani U., Costa R.H.;
RT "The transcriptional activator hepatocyte nuclear factor 6 regulates
RL liver gene expression.";
RL Mol. Cell. Biol. 16:6273-6284(1996).
CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS THE CONSENSUS SEQUENCE
CC OF HNF3B AND TTR. IMPORTANT FOR LIVER GENES TRANSCRIPTION. THE
CC AFFINITY OF HNF-6ALPHA AND HNF-6BETA FOR DNA DIFFERS DEPENDING ON
CC THE TARGET SEQUENCE.
CC -!- SUBUNIT: BINDS DNA AS A MONOMER.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BRAIN, SPLEEN AND TESTIS.
CC -!- SIMILARITY: CONTAINS 1 CUT DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEBOX PROTEINS.
CC
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CC
CC EMBL: X96553; CAA65389.1; -
CC EMBL: Y14933; CAA75150.1; -
CC TRANSFAC: T03257; -
CC TRANSFAC: T03258; -
CC InterPro: IPR003350; CUT.
CC InterPro: IPR001356; Homeobox.
CC Pfam: PF02376; CUT; 1.
CC Pfam: PF00046; homeobox; 1.
CC SMART: SM00389; HOX; 1.
CC PROSITE: PS00027; HOMEBOX_1; FALSE_NEG.
CC PROSITE: PS00071; HOMEBOX_2; 1.
CC Transcription regulation: Homeobox; DNA-binding; Nuclear protein;
KW Activator; Alternative splicing.
FT DNA_BIND 283 369 CUT
FT DNA_BIND 385 444 HOMEBOX.
FT DOMAIN 69 72 POLY-HIS.
FT DOMAIN 124 138 POLY-HIS.
FT DOMAIN 455 460 POLY-SER.
FT VARSPPLIC 368 368 A -> AESAMGSSVPSLRITSGGQQLSVPPPLP (IN
FT ISOFORM BETA).
SQ SEQUENCE 465 AA; 51067 MW; BD651267FD7AC896 CRC64;

Query Match 8.0%; Score 85.5; DB 1; Length 465;
Best Local Similarity 25.8%; Pred. No. 1;
Matches 48; Conservative 14; Mismatches 53; Indels 71; Gaps 11;

OY 18 AHDPSLRGPHSHGTHPCYSAEELPLGQAPP-----HLLARGAKWGQALPVLYSSLEA 72

Db 220 AHPHAMLGRHGEQHLTP--TSAGMVPINGLPPHPHHLNAQGG--HGQLLGTG----- 268
OY 73 ASHRGRHERPSAT-----TQCPVLRPPEVLEADTHQRSISFWRYRVDTDREY-- 120
Db 269 -----REPNSVPTGAQVNSGNGMEEINTKEVAQ-----RIITLEKRYSI 310
OY 121 POKLAFACLCR--GCID-----ARTGRETAALNSVRL-----LQSLVLVR 159
Db 311 PQAIFAQRVLCHRSQGLDLSLLRNPKWPKLKSRETFR-----RMWKWLOEPEFORMSALR 366
OY 160 RPPCSR 165
Db 367 LAACKR 372
RESULT 15
BRM_DROME
ID BRM_DROME STANDARD; PRT; 1638 AA.
AC P25439; Q9VUW5; Q9VUW6;
DT 01-MAY-1992 (Rel. 22, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Homeotic gene regulator (Brahma protein).
GN BRM OR CG5942 OR CG18438.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RX MEDLINE=92154670; PubMed=1346755;
RA Tankun J.W., Deuring R., Scott M.P., Kissinger M., Pattatucci A.M.,
RA Kaufman T.C., Kennison J.A.;
RT "Brahma: a regulator of Drosophila homeotic genes structurally
RT related to the yeast transcriptional activator SNF2/SWI2.";
RL Cell 68:561-572(1992).
RN [2]
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe W., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.M., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2193(2000).
CC -!- FUNCTION: MAY ACT AS COACTIVATOR, ASSISTING ONE OR MORE DEDICATED
CC TRANSCRIPTIONAL ACTIVATORS OF ANT-C AND BX-C HOMEOTIC GENES. CAN
CC COUNTERACT THE REPRESSIVE EFFECT OF POLYCOMB PROTEIN.
CC -!- SUBCELLULAR LOCATION: Nuclear
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- DEVELOPMENTAL STAGE: HIGHEST EXPRESSION IN UNFERTILIZED EGGS AND
CC EARLY EMBRYOS.
CC -!- MISCELLANEOUS: 'BRAHMA' MEANS 'FATE' IN INDIA.
CC -!- SIMILARITY: CONTAINS 1 BROMODOMAIN.
CC -!- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
CC -----
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CC -----
DR EMBL; M85049; AAA19661.1; -;
DR EMBL; AE003529; AAF49557.1; -;
DR EMBL; AE003529; AAF49558.2; -;
DR PIR; A42091; A42091.
DR FlyBase; FBgn0000212; brm.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR000330; SNF2_N.
DR Pfam; PF00439; bromodomain; 1.
DR Pfam; PF00271; helicase_C; 1.
DR Pfam; PF00176; SNF2_N; 1.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00297; BROMO; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICCC; 1.
DR PROSITE; PS00633; BROMODOMAIN_1; 1.
DR PROSITE; PS00614; BROMODOMAIN_2; 1.
KW Developmental protein; Transcription regulation; Nuclear protein;
KW Activator; Bromodomain; Helicase; ATP-binding; Alternative splicing.
FT DOMAIN 201 390 GLN/PRO-RICH.
FT NP_BIND 798 805 ATP (POTENTIAL).
FT SITE 900 903 DEGH BOX.
FT DOMAIN 1385 1392 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 1394 1404 ARG/LYS-RICH (BASIC).
FT DOMAIN 1405 1410 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 1415 1432 ARG/LYS-RICH (BASIC).
FT DOMAIN 1443 1513 BROMODOMAIN.
FT DOMAIN 1631 1638 POLY-ASP.
FT VARSPLIC 121 121 G -> A (IN SHORT ISOFORM).
FT VARSPLIC 122 222 MISSING (IN SHORT ISOFORM).
FT CONFLICT 687 687 D -> Y (IN REF. 1).
SQ SEQUENCE 1638 AA; 185088 MW; A4494B29F4F2E42A CRC64;

Query Match 7.9%; Score 84.5; DB 1; Length 1638;
Best Local Similarity 22.2%; Pred. No. 5.2;
Matches 42; Conservative 26; Mismatches 70; Indels 51; Gaps 8;
QY 22 PSLRGPHSHGTPHCYSAEELPLGQAPPH-----LIARGAKWGQALPVALVSSLEAASHRG 77
DB 52 PGAYGHPMQHGPP-----GQPGCHHPPHGHQMFISKGP HMGQMP---PTGFNMSPYQT 104
QY 78 RHERPSATTCQCPVLR-----PEEVLEADTH--QRSISPWRYRVDTDDEDRYPKLA 125
DB 105 HGMPPNAPTQPCIVSPGPGPPGPPPPSSQENLHALQRAIDSMEEKGLQEDPRYSQLLA 164

QY 126 FAELCLRCGICIDARTGRTAALNSVRLIQS-----LLVLRRRPCSRD----- 166
DB 165 -----MRATSKHOHLNGNQVNLRLTQITAYRLLARNKPIISMOMQQAALAAQQQPPPP 215
QY 167 GSGLPTPGA 175
DB 216 GPPIGPPGA 224

Search completed: August 23, 2002, 16:02:33
Job time: 98 sec

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OM protein - protein search, using sw model

Run on: August 23, 2002, 16:00:54 ; Search time 19.69 Seconds
(without alignments)
961.381 Million cell updates/sec

Title: US-09-854-208-3
Perfect score: ~ 1073
Sequence: 1 MTLLPGLLFTWLHTCLAH.....FHTEFHVPVGCTCVLP RSV 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	160.5	15.0	151	B45351	immediate-early pr
2	148.5	13.8	147	JC4628	cytotoxic T-lympho
3	148.5	13.8	150	I49623	cytotoxic T-lympho
4	110	10.3	148	T21334	hypothetical prote
5	93.5	8.7	395	K1SMG	galactokinase (EC
6	86.5	8.1	389	T50809	hypothetical prote
7	86	8.0	297	JL0032	hypothetical 31.7K
8	84.5	7.9	1638	A42091	transcription acti
9	82.5	7.7	635	T76371	hypothetical prote
10	81.5	7.6	325	T23218	hypothetical prote
11	81	7.5	553	D83640	hypothetical prote
12	80.5	7.5	210	B40203	4-alpha-glucanotra
13	80	7.5	411	A70509	hypothetical prote
14	79.5	7.4	638	JC7753	ring finger B-box
15	79	7.4	549	I37386	fas-activated seri
16	79	7.4	837	T12514	hypothetical prote
17	79	7.4	885	T57894	hypothetical prote
18	78.5	7.3	132	E27203	hypothetical prote
19	78	7.3	309	T37033	hypothetical prote
20	77.5	7.2	209	T30698	hypothetical prote
21	77.5	7.2	323	A35909	fra-2 protein - ch
22	77.5	7.2	567	E96784	ethylene-insensiti
23	77	7.2	420	T14166	fxuD protein - Msc
24	77	7.2	466	T36212	replication initia
25	77	7.2	639	T97670	beta-n-acetylhexos
26	77	7.2	639	AC2895	beta-N-acetylhexos
27	76.5	7.1	405	G84338	3-hydroxy-3-methyl
28	76.5	7.1	503	S64787	pre-mRNA splicing
29	76.5	7.1	1882	T00069	hypothetical prote

ALIGNMENTS

RESULT 1

B45351
Immediate-early protein 2 - saimirine herpesvirus 1 (strain 11)
N:Alternate names: hypothetical protein ORF13
C:Species: saimirine herpesvirus 1
A:Note: host Saimiri sciureus (common squirrel monkey)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: B45351; D36807
R:Nicholas, J.; Smith, E.P.; Coles, L.; Honess, R.
Virolgy 179, 189-200, 1990
A:Title: Gene expression in cells infected with gammaherpesvirus saimiri: properties
A:Reference number: A45351; MUID:91021021
A:Accession: B45351
A:Molecule type: mRNA
A:Residues: 1-151 <NIC>
A:Cross-references: GB:M60286; NID:g331040; PIDN:AAA46156.1; PID:g331042
R:Albrecht, J.
submitted to the EMBL Data Library, January 1992
A:Description: Primary structure of the herpesvirus saimiri genome.
A:Reference number: A36806
A:Accession: D36807
A:Molecule type: DNA
A:Residues: 1-151 <ALB>
A:Cross-references: GB:X64346; NID:g60320; PIDN:CAA45636.1; PID:g60334
R:Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.;
J. Virol. 66, 5047-5058, 1992
A:Title: Primary structure of the herpesvirus saimiri genome.
A:Reference number: A37309; MUID:92333688
A:Contents: annotation: protein-coding frames
A:Note: neither protein nor nucleotide sequence is given
C:Genetics:
A:Gene: 13
C:Superfamily: saimiri herpesvirus immediate-early protein 2
C:Keywords: early protein

Query Match 15.0%; Score 160.5; DB 1; Length 151;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAAASHRGHERPSATTQCPVLRPE 95
DB 18 CIVKSEIYSAQTPRCCLAA-----NNSFPRSVMTLSIRNWTSSKRAS----- 60
QY 96 VLEADTHORISPMRYVDTDDEYRYPQKLAFACLCRCIDARTGRTAALNSVRLQSL 155
DB 61 ----DYNNRSTSPWTLHRNQDQDRYPSVWEAKRYLGCVNA-DGNVDYHMSVPIQEEI 115
QY 156 LVLR--RPCSRDGSLGTPPGAFATFTHVPGCTCVLP 194
DB 116 LVVRKGHPCPN-----SFRLEKMLVTGCTCTVP 145

probable oxidoredu
hypothetical prote
sensory box sensor
hypothetical prote
protein kinase (EC
hypothetical prote
CD27 antigen precu
hypothetical 37.5K
transcription fact
probable transcrip
hypothetical prote
probable ddla - My
iacta protein - Li
hypothetical prote
hypothetical prote
transcription fact

```

RESULT      2
JC4628
cytotoxic T-lymphocyte-associated antigen 8 precursor - mouse
N:Alternate names: CTLA8 protein
C:Species: Mus musculus (house mouse)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
C:Accession: JC4628
R:Yao, Z.; Timour, M.; Painter, S.; Fanslow, W.; Spriggs, M.
Gene 168, 223-225, 1996
A:Title: Complete nucleotide sequence of the mouse CTLA8 gene.
A:Reference number: JC4628; MUID:96194901
A:Accession: JC4628
A:Molecule type: DNA
A:Residues: 1-147 <YAO>
A:Cross-references: GB:U35108; NID:g1244499; PIDN:AAA93253.1; PID:g1244500
C:Genetics:
A:Gene: ctla8
A:Introns: 69/2
C:Superfamily: saimiri herpesvirus immediate-early protein 2
C:Keywords: cytokine; glycoprotein; lymphocyte
F:1-14/Domain: signal sequence #status predicted <SIG>
F:15-147/Product: cytotoxic T-lymphocyte-associated antigen 8 #status predicted <MAT>
F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      13.8%; Score 148.5; DB 2; Length 147;
Best Local Similarity 37.6%; Pred. No. 1.5e-06;
Matches 38; Conservative 13; Mismatches 35; Indels 15; Gaps 3;

QY  92 RPEVLEADTHORSISPRWYVDDEDRYPQKLAFAECLRGCIDARTGRETAALNSVRL 151
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   54 RPSDYL-----NRSTSPWTLHRNDDPRYPSVIAEQHORCVNAE-GKLDHMHNSVLI 107
    | : ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY  152 LQSLVLRRLRRPCSRDGSGLPTPGAFAFTEFIHVPVGCTCV 192
    | : ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   108 QQEILVLRKREPES-----CPFTRVEKMLVGVCCTCV 139
    | : ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT      3
I49623
cytotoxic T-lymphocyte-associated antigen 8 precursor - mouse
N:Alternate names: Immediate-early protein 2 (ORE13) homolog
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 26-Aug-1999
C:Accession: I49623
R:Rouvier, E.; Luciani, M.
J. Immunol. 150, 5445-5456, 1993
A:Title: CTLA-8, cloned from an activated T cell, bearing AU-rich messenger RNA instal
A:Reference number: I49623; MUID:93294300
A:Accession: I49623
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-150 <RES>
A:Cross-references: GB:U13839; NID:g293329; PIDN:AAA37490.1; PID:g293330
C:Genetics:
A:Gene: Ctla-8
C:Superfamily: saimiri herpesvirus immediate-early protein 2

Query Match      13.8%; Score 148.5; DB 2; Length 150;
Best Local Similarity 29.4%; Pred. No. 1.5e-06;
Matches 45; Conservative 20; Mismatches 55; Indels 33; Gaps 5;

QY  42 LPLGQAPPHLLARGAKWGQALPVALVSSLEASHRGHERPSATTQCVLRPEVLEADT 101
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   21 IPOSSVCPNAEANNFLQNKVNLKVINSL---SSKASSRRPS-----DY 61
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY  102 HQRSISPRWYVDDEDRYPQKLAFAECLRGCIDARTGRETAALNSVRLQSLVLRRL 161
    ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   62 LNRSTSPWTLHRNDDPRYPSVIAEQHORCVNAE-GKLDHMHNSVLIQEQILKRE 120
    | : ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY  162 P--CSRDSGLPTPGAFAFTEFIHVPVGCTCV 192

```

[illegible]

Db 303 A---ARRLPHLLP-RAGPGRRHGPGURGP 327

RESULT 6

T50809

hypothetical protein T30N20_270 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000

C:Accession: T50809

R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; New

submitted to the Protein Sequence Database, July 2000

A:Reference number: Z25240

A:Accession: T50809

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-389 <BEV>

A:Cross-references: EMBL:AL365234

A:Experimental source: cultivar Columbia; BAC clone T30N20

C:Genetics:

A:Map position: 5

A:Note: T30N20_270

Query Match 8.1%; Score 86.5; DB 2; Length 389;

Best Local Similarity 23.0%; Pred. No. 2.3;

Matches 56; Conservative 25; Mismatches 83; Indels 79; Gaps 10;

QY 6 GLLFLTLHTCLAHDPDSLRGHP---HSHGTHPCYSAEELPLGQAPP-HL-----LA----- 53

Db 44 GVFLYLTWSTFLGGHVNFLHSQDYNNHSSPLSFSSADLSVASFHLNLTAFWK 103

QY 54 RGAK-----WG-----QALPVALV-----SSLEAAASHRGRHER 81

Db 104 RGSREVPSPKIQVFWDLSKAKFDGSGSEPRSGFVIIVVDGEMGLLVGDSVKEAVARAKSAK 163

QY 82 PSATTQCPVLRPEEVLADTHORSISPWRYRYVDTDEDRYPQKLAFAECLRCGIDAR---- 138

Db 164 PPTNFQALLLRKEHVFGA-----RVFTTKAREFGGKNREITSIDCRVDEDAKLCF 211

QY 139 -----TGRETAALNSVRLQSLV---LRRPCSRDGGSLPTPGARAF 178

Db 212 SVDSKQVLQIKLRWKFNGKVEIDGVHVQISWDVYNWLFOSKSGDGGGGGHVAFMF 271

QY 179 HTE 181

Db 272 RFE 274

RESULT 7

JL0032

hypothetical 31.7K protein (aphE region) - Streptomyces griseus

C:Species: Streptomyces griseus

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Oct-1999

C:Accession: JL0032

R:Heinzel, P.; Werbitsky, O.; Distler, J.; Piepersberg, W.

Arch. Microbiol. 150, 184-192, 1988

A:Title: A second streptomycin resistance gene from Streptomyces griseus codes for strep

A:Reference number: JL0031; MUID:88339496

A:Accession: JL0032

A:Molecule type: DNA

A:Residues: 1-297 <HEI>

A:Cross-references: GB:M37378; GB:X56876; NID:g153162; PIDN:AAA26701.1; PID:g153164

A:Experimental source: strain N2-3-11

A:Note: the function of the protein is unknown; the orf1 gene and aphE (streptomycies-3"-

C:Genetics:

A:Gene: orf1

C:Superfamily: Streptomyces griseus hypothetical 31.7K protein (aphE region)

Query Match

Best Local Similarity 8.0%; Score 86; DB 2; Length 297;

Matches 40; Conservative 15; Mismatches 55; Indels 36; Gaps 7;

	Query Match	7.4%	Score 79.5;	DB 2;	Length 638;
	Best Local Similarity	30.3%;	Pred. No. 18;		
	Matches 36;	Conservative 10;	Mismatches 56;	Indels 17;	Gaps 6;
QY	40 EELPLGQAPPHLLARGAKWQALPVAL--VSSLEA--ASHRGHRHERPSATTQCVPVLURPEE	95			
DB	118 EPWAGEEP--VRCDACPGGAALPAALSCLSLASFCPAHLGHPHERSPALRGHRIYPPRLR	175			

Search completed: August 23, 2002, 16:02:16
Job time: 82 sec

Search completed: August 23, 2002, 16:02:16
Job time: 82 sec

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	173	16.1	153	1	US-08-514-014-12	Sequence 12, Appl	
2	173	16.1	153	2	US-08-833-823-12	Sequence 12, Appl	
3	173	16.1	163	3	US-09-034-810-2	Sequence 2, Appl	
4	173	16.1	163	3	US-08-685-239-2	Sequence 2, Appl	
5	160.5	15.0	151	2	US-08-620-694A-8	Sequence 8, Appl	
6	160.5	15.0	151	3	US-09-034-810-6	Sequence 6, Appl	
7	160.5	15.0	151	3	US-09-022-255-8	Sequence 8, Appl	
8	160.5	15.0	151	3	US-09-022-696-8	Sequence 8, Appl	
9	160.5	15.0	151	3	US-08-685-239-6	Sequence 6, Appl	
10	160.5	15.0	151	3	US-09-022-253-8	Sequence 8, Appl	
11	160.5	15.0	151	3	US-09-022-260-8	Sequence 8, Appl	
12	160.5	15.0	151	4	US-09-022-259-8	Sequence 8, Appl	
13	160.5	15.0	151	4	US-09-022-257-8	Sequence 8, Appl	
14	160.5	15.0	151	4	US-08-432-994A-4	Sequence 4, Appl	
15	158	14.7	155	4	US-08-432-994A-8	Sequence 8, Appl	
16	150.5	14.0	158	2	US-08-620-694A-7	Sequence 7, Appl	
17	150.5	14.0	158	3	US-09-022-255-7	Sequence 7, Appl	
18	150.5	14.0	158	3	US-09-022-696-7	Sequence 7, Appl	
19	150.5	14.0	158	3	US-09-022-253-7	Sequence 7, Appl	
20	150.5	14.0	158	3	US-09-022-260-7	Sequence 7, Appl	
21	150.5	14.0	158	4	US-09-022-259-7	Sequence 7, Appl	
22	150.5	14.0	158	4	US-09-022-257-7	Sequence 7, Appl	
23	148.5	13.8	150	3	US-09-034-810-4	Sequence 4, Appl	
24	148.5	13.8	150	3	US-08-685-239-4	Sequence 4, Appl	
25	148.5	13.8	150	4	US-08-432-994A-2	Sequence 2, Appl	
26	148.5	13.8	158	4	US-08-432-994A-10	Sequence 10, Appl	
27	125	11.6	179	4	US-08-432-994A-6	Sequence 6, Appl	

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Db 60 MSRNIESRSTSPWNYVTWDPNRYPSVVQACRNLCGINAQ-GKEDISMNSVPIQOETL 118
QY 157 VLRRR--PCSRDGSGLPTGCAFAFHTEFIHVPVGCCTCPLP 194
      :|||: || | : | ||||| |
Db 119 VVRKHQGC-----VSFQLEKVLVTGCTCVP 147

RESULT 2
US-08-833-823-12
; Sequence 12, Application US/08833823
; Patent No. 5969093
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,823
; FILING DATE: 10-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/514,014
; FILING DATE: 11-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G16000
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-823-12

Query Match 16.1%; Score 173; DB 2; Length 153;
Best Local Similarity 39.0%; Pred. No. 9.4e-13;
Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

QY 97 LEADTHQRSTSPWRYVDTEDEDRYPQKLAFAECLRCGCDARTGRTAALNSVRLQLSLL 156
      : || ||| | | : ||| : | : ||| : | : ||| : | |
Db 60 MSRNIESRSTSPWNYVTWDPNRYPSVVQACRNLCGINAQ-GKEDISMNSVPIQOETL 118
      : |||: || | : | ||||| |
QY 157 VLRRR--PCSRDGSGLPTGCAFAFHTEFIHVPVGCCTCPLP 194
      :|||: || | : | ||||| |
Db 119 VVRKHQGC-----VSFQLEKVLVTGCTCVP 147

RESULT 3
US-09-034-810-2
; Sequence 2, Application US/09034810
; Patent No. 6043344
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
```

```
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; APPLICANT: Goldman, Samuel
; APPLICANT: Pittman, Debra
; APPLICANT: Mi, Sha
; APPLICANT: Neben, Steven
; APPLICANT: Giannotti, JoAnn
; APPLICANT: Golden/Fleet, Margaret
; TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,810
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,239
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-034-810-2

Query Match 16.1%; Score 173; DB 3; Length 163;
Best Local Similarity 39.0%; Pred. No. 1e-12;
Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

QY 97 LEADTHQRSTSPWRYVDTEDEDRYPQKLAFAECLRCGCDARTGRTAALNSVRLQLSLL 156
      : || ||| | | : ||| : | : ||| : | : ||| : | |
Db 70 MSRNIESRSTSPWNYVTWDPNRYPSVVQACRNLCGINAQ-GKEDISMNSVPIQOETL 128
      : |||: || | : | ||||| |
QY 157 VLRRR--PCSRDGSGLPTGCAFAFHTEFIHVPVGCCTCPLP 194
      :|||: || | : | ||||| |
Db 129 VVRKHQGC-----VSFQLEKVLVTGCTCVP 157

RESULT 4
US-08-685-239-2
; Sequence 2, Application US/08685239
; Patent No. 6074849
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; APPLICANT: Goldman, Samuel
; APPLICANT: Pittman, Debra
; APPLICANT: Mi, Sha
; APPLICANT: Neben, Steven
; APPLICANT: Giannotti, JoAnn
; APPLICANT: Golden/Fleet, Margaret
; TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
```

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,239
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-685-239-2

Query Match 16.1%; Score 173; DB 3; Length 163;
Best Local Similarity 39.0%; Pred. No. 1e-12; Indels 14; Gaps 3;
Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;
QY 97 LEADTHORSISPRWYRVDTDEDPQKLAFAECLRCGICIDARTGRTAALNSVRLQLL 156
DB 70 MSRNIESRSTSPWTVTVDNRYSEVVQACRNLGCINAQ-GKEDISMSVPIQOETL 128
QY 157 VLRRR--PCSRDGSGLPTPGAFAFHTEFIHVPVGTCTVLP 194
DB 129 VYRRKHGCS-----VSFOLEKVLVTGCTCTVTP 157

RESULT 5
US-08-620-694A-8
Sequence 8, Application US/08620694A
Patent No. 5869286
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: NO. 5869286el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Herpesvirus Saimiri
STRAIN: ORE13
US-08-620-694A-8

Query Match 15.0%; Score 160.5; DB 2; Length 151;
Best Local Similarity 28.6%; Pred. No. 2.8e-11;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;
QY 36 CYSAEPLPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRHERPSATTQCPVLRPEE 95
DB 18 CIVKSEITSAQPPRCIAA-----NNSFPRSVMTLSIRNWTSSKRAS----- 60
QY 96 VLEADTHORSISPRWYRVDTDEDPQKLAFAECLRCGICIDARTGRTAALNSVRLQLL 155
DB 61 ----DYNNRSTSPFWLHRNEDQDRYPSVIWEAKCRYLGCVNA-DGNVDYHMSVPIQOEI 115
QY 156 VLRRR--PCSRDGSGLPTPGAFAFHTEFIHVPVGTCTVLP 194
DB 116 LVVRKHGQCPN-----SFRLEKMLVTGCTCTVTP 145

RESULT 6
US-09-034-810-6
Sequence 6, Application US/09034810
Patent No. 6043344
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: Kelleher, Kerry
APPLICANT: Carlin, McKeough
APPLICANT: Goldman, Samuel
APPLICANT: Pittman, Debra
APPLICANT: Mi, Sha
APPLICANT: Neben, Steven
APPLICANT: Giannotti, JoAnn
APPLICANT: Golden/Fleet, Margaret
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,810
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/685,239
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15/262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-034-810-6

Query Match 15.0%; Score 160.5; DB 3; Length 151;
Best Local Similarity 28.6%; Pred. No. 2.8e-11;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGHRHPSATTQCPVLRPEE 95
DB 18 CIVKSEITSAQTPRCCLAA-----NNSFPRSVMTLSIRNMTSSKRAS----- 60

QY 96 VLEADTHQRSISPWRYRVDDEDRYPQKLAFAECLRCGICDARTGRETAALNSVRLQSL 155
DB 61 ----DYNNRSTSPWTLHRNEDQDRYPSVIWEAKRYLGCVNA-DGNVDYHMSVPIQOEI 115

QY 156 LVLR--RPCSRDGSGLPTPGAFATFTHVPVGCTCVLP 194
DB 116 LVVRKGHPQCPN-----SFRLEKMLVTGCTCTVTP 145

RESULT 7
US-09-022-255-8
; Sequence 8, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpesvirus Saimiri
; STRAIN: ORF13
; US-09-022-255-8

Query Match 15.0%; Score 160.5; DB 3; Length 151;
Best Local Similarity 28.6%; Pred. No. 2.8e-11;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGHRHPSATTQCPVLRPEE 95
DB 18 CIVKSEITSAQTPRCCLAA-----NNSFPRSVMTLSIRNMTSSKRAS----- 60

QY 96 VLEADTHQRSISPWRYRVDDEDRYPQKLAFAECLRCGICDARTGRETAALNSVRLQSL 155
DB 61 ----DYNNRSTSPWTLHRNEDQDRYPSVIWEAKRYLGCVNA-DGNVDYHMSVPIQOEI 115

QY 156 LVLR--RPCSRDGSGLPTPGAFATFTHVPVGCTCVLP 194
DB 116 LVVRKGHPQCPN-----SFRLEKMLVTGCTCTVTP 145

RESULT 8
US-09-022-696-8
; Sequence 8, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535

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; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpesvirus Saimiri
; STRAIN: ORF13
; US-09-022-696-8

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Query Match	15.0%	Score 160.5;	DB 3;	Length 151;
Best Local Similarity	28.6%;	Pred. No. 2.8e-11;		
Matches	46;	Conservative 23;	Mismatches 57;	Indels 35; Gaps 5;
QY	36	CYSAEEPLGQAPHLIARGAKWGOALPVALLVSSLEAASHGRGHRPESATTQCPVLRPEE	95	
Db	18	CIYKSEITSATQTPCLAA-----NNSPFRVVMVTLSTRNWNTSSKRAS-----	60	
QY	96	VLEADTHORSTPMRYRVDTDEDYRPOKLAFAECLRGCIDARTGRETAAALNSVRLLOSL	155	
Db	61	----DYNRSTSPWTLHRNEDODRYPVSIWEAKCRYLGCVNA-DGNVDYHMNSVP IQOEI	115	
QY	156	LVLR--R-PCSRDGGSLPTPGAFATHEFTTHVPVGCCTCLVP	194	
Db	116	LVVRKGHQPCPN-----SFRLEKMLVTVGCTCVTP	145	

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RESULT      9
US-08-685-239-6
; Sequence 6, Application US/08685239
; Patent No. 6074849
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; APPLICANT: Goldman, Samuel
; APPLICANT: Pittman, Debra
; APPLICANT: Mi, Sha
; APPLICANT: Neben, Steven
; APPLICANT: Giannotti, JoAnn
; APPLICANT: Golden/Fleet, Margaret
; TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,239
; FILING DATE:
; CLASSIFICATION: 435

```

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: ATTORNEY/AGENT INFORMATION:
: NAME: Brown, Scott A.
: REGISTRATION NUMBER: 32.7
: REFERENCE/DOCKET NUMBER:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 498-8224
: TELEFAX: (617) 876-5951
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 151 amino acid
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-685-239-6

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Query Match	15.0%	Score 160.5;	DB 3;	Length 151;
Best Local Similarity	28.6%;	Pred. No. 2.8e-11;		
Matches	46;	Conservative 23;	Mismatches 57;	Indels 35; Gaps 5;
Qy	36	CYSAEELPLGQAPHLLARGAKWQALPVALVLSLEAASHRGHERPSATTQCPVL	RPEE	95
Db	18	CIYKSEITSQTPCLAA-----NNSPRVVMVTLSTRNWNTSSKRAS-----		60
Qy	96	VLEADTHQRSTWRYRVDTHDEQYPOKLAFAECLRGCIDARTGRETAALNSVRLQLS		155
Db	61	----DYNNRSTSPWTLHRNEDQDQYPSVWEAKCRYLGCVNA-DGNVDYHMNSVP	IQOEI	115
Qy	156	LVLRR--RPSCRDGSGLPTPGCAFATHTFEFTHVPVGCTCVLP		194
Db	116	LVRKKGHPQCPN-----SFRLEKMLVTVGCTCVTP		145

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RESULT 10
US-09-022-253-8
; Sequence 8, Application US/09022253
; Patent No. 6096305
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION NUMBER: US/09/022,253
; APPLICATION NUMBER: US/09/022,253
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694
; FILING DATE: 21-MARCH-1996
; APPLICATION NUMBER: USN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B

```

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. 6096305 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpesvirus Saimiri
; STRAIN: ORF13
;
US-09-022-253-8
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Query Match 15.0%; Score 160.5; DB 3; Length 151;
Best Local Similarity 28.6%; Pred. No. 2.8e-11;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGHRERPSATTQCPVLRPEE 95
Db 18 CIVKSEITSAQTPRCCLAA-----NNSFPRSVVMVTLIRNWTSSKRAS----- 60

QY 96 VLEADTHORSISPWRYRVDTDDEYPOKLAFAECLRCGICDARTGRTAALNSVRLQLSL 155
Db 61 ---DYNNRSTSPWTLHRNEDQDRYPSVIWEAKCRYLGCVNA-DGNVDYHMNSVP IQEI 115

QY 156 LVLR--RPCSRDGSGLPTPGAFATFTHIVPVGCTCVLP 194
Db 116 LVVRKGHQPCPN-----SFRLEKMLVTVGCTCVTP 145
```

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RESULT 11
US-09-022-260-8
; Sequence 8, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
```

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpesvirus Saimiri
; STRAIN: ORF13
;
US-09-022-260-8

Query Match 15.0%; Score 160.5; DB 3; Length 151;
Best Local Similarity 28.6%; Pred. No. 2.8e-11;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLEAASHRGHRERPSATTQCPVLRPEE 95
Db 18 CIVKSEITSAQTPRCCLAA-----NNSFPRSVVMVTLIRNWTSSKRAS----- 60

QY 96 VLEADTHORSISPWRYRVDTDDEYPOKLAFAECLRCGICDARTGRTAALNSVRLQLSL 155
Db 61 ---DYNNRSTSPWTLHRNEDQDRYPSVIWEAKCRYLGCVNA-DGNVDYHMNSVP IQEI 115

QY 156 LVLR--RPCSRDGSGLPTPGAFATFTHIVPVGCTCVLP 194
Db 116 LVVRKGHQPCPN-----SFRLEKMLVTVGCTCVTP 145
```

```
RESULT 12
US-09-022-259-8
; Sequence 8, Application US/09022259
; Patent No. 6191104
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,259
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Herpesvirus Saimiri
STRAIN: ORF13
US-09-022-259-8

Query Match 15.0%; Score 160.5; DB 4; Length 151;
Best Local Similarity 28.6%; Pred. No. 2.8e-11;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;
QY 36 CYSAEPLGQAPPHLLARGAKWGQALPVALLYSSLEAASHRGHERPSATTQCPVLRPEE 95
DB 18 CIVKSEITSAQTPRCCLAA-----NNSFPRSVMTLSIRNWTSSKRAS----- 60
QY 96 VLEADTHORSISPRWRYVDTDDEDRYPQKLAFAECLRCGICDARTGRETAALNSVRLQSL 155
DB 61 ----DYNNSTSPWTLHRNEDQDRYPSVIWEAKCRYLGCVNA-DGNVDYHMSVPVQOEI 115
QY 156 LVLR--RPCS RDGSLPTPGAFATHTFIHVPVGCCTVLP 194
DB 116 LVVRKGHPQCPN-----SFRLEKMLVTGCTCTVP 145

RESULT 13
US-09-022-257-8
Sequence 8, Application US/09022257
Patent No. 6197525
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
FILING DATE: US/09/022,257
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Herpesvirus Saimiri
STRAIN: ORF13
US-09-022-257-8
Query Match 15.0%; Score 160.5; DB 4; Length 151;
Best Local Similarity 28.6%; Pred. No. 2.8e-11;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;
QY 36 CYSAEPLGQAPPHLLARGAKWGQALPVALLYSSLEAASHRGHERPSATTQCPVLRPEE 95
DB 18 CIVKSEITSAQTPRCCLAA-----NNSFPRSVMTLSIRNWTSSKRAS----- 60
QY 96 VLEADTHORSISPRWRYVDTDDEDRYPQKLAFAECLRCGICDARTGRETAALNSVRLQSL 155
DB 61 ----DYNNSTSPWTLHRNEDQDRYPSVIWEAKCRYLGCVNA-DGNVDYHMSVPVQOEI 115
QY 156 LVLR--RPCS RDGSLPTPGAFATHTFIHVPVGCCTVLP 194
DB 116 LVVRKGHPQCPN-----SFRLEKMLVTGCTCTVP 145
RESULT 14
US-08-432-994A-4
Sequence 4, Application US/08432994A
Patent No. 6274711
GENERAL INFORMATION:
APPLICANT: Golstein, Pierre
APPLICANT: Rouvier, Eric
APPLICANT: Fossiez, Francois
APPLICANT: Lebecque, Serge J.E.
APPLICANT: Diossou, Odile
APPLICANT: Banchereau, Jacques
TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-8 ANTIGENS AND
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,994A
FILING DATE: 02-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/250,846
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/177,747
FILING DATE: 05-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,203

